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Point of Contact:  
Barb O'Bryen  
Technical Information Specialist  
STIC CM1 6A05 308-4291

Searcher: Paul Schulwitz / BOB  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 12-30-02  
Searcher Prep/Review: \_\_\_\_\_  
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Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

STIC CMU 1000 2000  
Technical Information Board  
Help & Power  
Form of 1000



Db	189	GGGACCTGGCGGGCGGCAAGTGGCGAAAGTGGAGTGTGGAGCTGGACACAGCTGCCG	248
Qy	229	GAGCAGCCGCTCTTCCTTGGCCGCTCAACCGCGGCT--CTGACCTTCCCGTGGCCG	285
Db	249	GAGCAGCGGCTCTTCCTTCGCGCGCGCTCCGCGCCGCGCCCACTCTTCCTCCGTCGCG	308
Qy	286	GAGCCCGCGAGCAGCGAGCGGGAGTGGGAGCCGGCTTCACAGCTTTGGCGGTGGCGGCC	345
Db	309	GAGCCCGGGAGACGGGCTGCAGAGAGCGAATGCTTCCAGCCCGCGGGACCGCACC	368
Qy	346	CACGAGCCGCGAGCCCGCGCGGCCCACTTACCGAGTGGTGGCGGCCCGGACAGC	405
Db	369	CCGGAGCGCGAGTCCCTGGCGCTCCCACTTCGCGAGCTGGCGCGCCGCGGGACAGC	428
Qy	406	GAGCGCTGAGTCCCGGAGCGGCCGAGCCGGGGAGAAAGCGGGCGGCCCGCCAGACCG	465
Db	429	GGCGCCCGAGCCCCGGGGG-----CGGAGCGG	458
Qy	466	TCTCCTGCAGCGCCCCCGCGGCTGAGATGAGAAATAAGCACTCAAGAGGTG	525
Db	459	CCCTCTGCAGCGGCCCTCCGCGGCGAGAGATGAGAAATAAGAAACCTCAAGGACAG	518
Qy	526	CACAAGATGATGATCTCTCCAGAGGAACAATATCAGGAGAACTGAAGCAACTGT	585
Db	519	CACAAGATGAGATGCTCCCGGAGAGAAATATCCGGAGAACTCAAGCGACACTGT	578
Qy	586	ATCGCAGCCTGGAAGCACGAATGTTGGAAGAGAAATAGCGGAGCGGCTGGGAGTA	645
Db	579	ATCCCGCGCTGGAAGCACAGATGTTTGAAGAGAGAACAGAGAGAGGCGCTGGTGGTG	638
Qy	646	AAACCAATCCAGTTAAAGAGATGATCTGAAATGATCATTTAGCAGCTGAGTCTCA	705
Db	639	AAGCCAACTCTATTAAAGGAGATGATCTGAAGTAAATTACTTGGCAGCTAGGCCAG	698
Qy	706	GGAGAGGTCGAGGGAAGGGGGCTTCACAGCTTCCAAAGCGCGAGCGAGCTCTCTCT	765
Db	659	GGAGAGGGCCAGGAGGTTCCGCTGCACACGCCCCCAAGGGCGAGAGGCCCATCTCT	758
Qy	766	GGCAACTCCCATCAGGTGCGACAGTGAATCAAAATCTTCAGAGTAAGGAGAAAAAG	825
Db	759	GGCAGCTCTCCGTGAGGGCGCTCGGTGAACCCGGAATCCCAAGAGTAAGACGAAAG	818
Qy	826	GTTTCCCGAGGCTTTCAGAGTGGAGAAATACACACACCCGAGACCCCTTACCA	885
Db	819	GTGTCCCGGCTCTTCAGAGTGGAGATACACACCCGAGAGCCCATCACC	878
Qy	886	GATGGCTTTCACCATATATACCCGTGAGAGAAACAACCGCGCTTAAACAATGTATCGG	945
Db	879	GATGGCTTTCCTCCGCTACAGCCAGAGAGAGAGCGCGCGGTGAACAATGATGAGA	938
Qy	946	GCCAGACTGTAATTAAGTACGACAGATATAGGCGCTTAATCTTTCTGATGGAGAGAC	1005
Db	939	GCCAGGCTGTACCGTGCAGACAGATATAGACCCCACTTCTGTGATGGAGAGACGT	998
Qy	1006	CCAGACAATAATACCGGGTATTATGGGCTTCACAACGTGACGCTGACGTGGAGACA	1065
Db	999	CCAGACAATAATACCGGGTATTATGGGCTTCACAACGTGACGCTGAGGTGAGACA	1058
Qy	1066	TTCGTATTCATCTGTAATTTGATGCTCGGGTGTTCACATAGAACCTTCAGACCA	1125
Db	1059	TTCGTATTCATCTGTAATTTGATGCTCGGGTGTTCACATAGAACCTTCAGACCC	1118
Qy	1126	ATGTTATGGAGAAAACTTTTAAAGAAATTTGAGAGTTGATGATCAGAAATATCAC	1185
Db	1119	ATGTTATGGAGAAAACTTTTAAAGAAATTTGAGAGTTGATGATCAGAAATATCAC	1178
Qy	1186	AGTAGGCTAGCTCAAGATCAAAAGCTCATCTGCTAACAACATCAGAAAGTTGTCTCA	1245
Db	1179	AGTAGGCTAGCTGAGAAATCAAAAGCTCATCTCCGGAGACCAATCCAGAAAGTTGTCTCA	1238
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Db	1239	CGATGTCAATTTCTCACACACACGTCTACTGCTGTACACATCCCACTATGTTTCACAAAAC	1298
Qy	1306	AGCATTAAGAATGGAAGAGAAACAGATGTCTCTATTTGCTTGTGGGCATGCTTATGAA	1365
Db	1299	AGCATCAAGAGATGGAAGAGAGACATATGTCTCCATCTGCTGTGGCATGCTGTGATAG	1358
Qy	1366	GAATCTCTTACAGTGTGTGAAGAGGGGTGGAGAACAGCTGCACACACATGACATGACA	1428
Db	1355	GAGAGCTGACTGTGTGTGAAGATGGCTGCAGAGAACAGTGCACACCATTTGATGTC	1418
Qy	1426	ATTGGGCAGAAAGAGTGTAGAAAGAAATAGAAACCTTAATATGTCCTCCCTTGTAGATCT	1485
Db	1419	ATCTGCGCGGAAGAGTGTAGAAAGAAATAGAGACCTTTAATATGTCCTCTTGTAGATCT	1478
Qy	1486	AAGTGAATCTCCATGTACTTCTACAGCCATGAGATTTATCAAGCCCTGTGAATGTCCTCCGCT	1538
Db	1479	AAGTGAATCTCCATGTACTTCTACAGCCATGAGATTTATCAAGCCCTGTGAATGTCCTCCGCT	1538
Qy	1546	TCCCTCAGAGCTGCACAGACAGCAACCCGTACACACAGCCCTTGGCTGTAGTCA--GGA	1602
Db	1539	TCCCTCAGAGCTGCACAGACAGCAACCCGTACACACAGCCCTTGGCTGTAGTCA--GGA	1598
Qy	1603	AGGAATCAAGAGACCAATTTTAACTTACTCATTTATGAACTCAGCAATCCCTCTGCT	1667
Db	1599	AGGAATCAAGAGACCAATTTTAACTTACTCATTTTGAACCCAGCAGATGCTTCCCT	1658
Qy	1663	TACAAAGATTTAGGTGAGCCATGAGATTCAGGTCTTTGGAAATGGAAATCGTGTGGCTGTTA	1722
Db	1659	TACAAAGATTTAGGTGAGCCATGAGATTCAGGTCTTTGGAAATGGAAATCGTGTGGCTGTTA	1718
Qy	1723	TTTTCTPAGAACTGGAATGTGAGAGAGATGGCCCTCAGCGCTTTCCTCCATGATGTCACT	1782
Db	1719	TTTTCTPAGAACTGGAATGTGAGAGAGATGGCCCTCAGCGCTTTCCTCCATGATGTCACT	1778
Qy	1783	GGGGCCCGTGTGGGAATGGGGAGACAGCTGGAATTCGTGGGGCAGCATGTGAAGC	1844
Db	1779	GGGGCCCGTGTGTGGGAAGGGGGAGACATGTGAAGACTGTGGAGCGGGCAGTGGGGC	1838
Qy	1843	AGCCGAGTGGGGAGGCCACCACTGAGGGTCTTCCCAAGCAGTATCTCAGAGAAATGTGTG	1902
Db	1839	AGCTTAACCGGGAGCGGCAGAGGGGTCTCCACGCCAGCATCTCAGGGATGTGGTG	1898
Qy	1903	GAGGATGCTCTACACCTTCTGTCAATAGTGTGTGTCTGACCCCTGTCTACAAATGTACGTT	1966
Db	1899	GAGGATGCTCTACACCTTCTGTCTATAGTGTGTGTGTGTGTCTCTACAAATGTACGTT	1958
Qy	1963	GCTGCTTTAAAAACATTGAGAGCCATGCTGTATATCTCTTGGCCAGCAGTTTACGGGA	2022
Db	1959	GCTGCTTTAAAAACATTGAGAGCCATGCTGTATATCTCTTGGCCAGCAGTGTGGCAGAA	2018
Qy	2023	AGAAATCAACTTCAGAGACTTCTCCAGCCAGTGTGAGACCACTCTACTCAATATGTGCA	2082
Db	2019	AGAAATCAACTTCAGAGACTTCTCCAGCCAGTGTGAGACCACTATCCTTCTCAAGTGTGCA	2078
Qy	2083	GATGCAATTAACCCGACAAAGCAGCTGTCCATTTCAACACTGTGGAACTGTGCAAAAGC	2142
Db	2079	GATGCAATTAACCCGACAAAGCAGCTGTCCATTTCAACACTGTGTGAATCTGTCAAAAGC	2138
Qy	2143	CAAGCAGAGAGTGGCAGAGTGTGGCAGAAATCTTAAAGCTGTGAGCCATTTGTATTTGCT	2202
Db	2139	CAAGCAGAGAGTGGCAGAGTGTGGGAGGAATCTTAAAGCTGTGGTCCATCGGGTGTGT	2198
Qy	2203	GGTGTATTATGTCTTAAATTTGATTTCTTGGAAACCAACTGAAATCAACATTTGGCA	2262
Db	2199	GGTGTCAATTACGCTTAAATTTGATTTCTTGGAAACCAAGCTGAATCAACATTTGGCA	2258
Qy	2263	GAACCTCTTGGCCCTTTGTCTTATAGATAGACCTTGTGTGGAAATTTCTGCTCAATTTT	2322
Db	2259	GAACCTCTTGGCTCCCTCTGTCTTATAGACAGGTTCTGTGTGAATTTCTCTCAATTC	2318
Qy	2333	TATCTCATATTTGCTACTGATGATTTTTCACAAAGCTGAGCCTGTGTGAATCAGTATAG	2382
Db	2319	TATCTCATATTTGCTACTGATGATTTTTCACAAAGCTGAGCCTGTGTGAATCAGTATAG	2378



QY	2283	AAAGTGTGTCTCTTTAAACCTTTGCTTTGACGTCCATTGATTTATTCACATGATGTT	2442
Db	2379	AAAGTGTCTCTCTCTTAAACCTTTGCTTTGACGTCCATTGATTTATTCACATGATGTT	2438
QY	2443	GGCAAACTTTTCCGAAGAGATCTACTTGGAGTCTTGGCAAGAAAGGTTTACTAGATGCCCAT	2502
Db	2439	GGCAAGCTCTCTCTGGAGGATATATCTGAACTTCTGCCAGAGATGTGTACCGCAATGCCCT	2498
QY	2503	GTTGTTTTCAAAACCTGTTAGAAATGCTGAAGTGTGTTCCAGTTCACATTCACATTAACAGATG	2562
Db	2499	GTTGTTTTCAAAAGCTGGTAAACCATGCTTAATTCGCTTCGGCTCACCACTTCAACAGATG	2558
QY	2563	CGTCCCGCTTTGATAGCGCTATGTAGATGAGGTGGAAATTTGCCGAAGCATCCAGTTGGCC	2622
Db	2559	CGCCGGGCTGTGATGGCTATCCGGGATGTGAGTAAGAAATTTGCCAGATCATCCACTGGGT	2618
QY	2623	GTAACAACACTTTGGATGGGTCAACAGGACACTTCTTGGACAGCATTCGTTCCACAAC	2682
Db	2619	GTTGAGGACACTGTGGATGGGATTCAGGACAG---CTTACAGGCCGTGGCCCCACCAAGC	2675
QY	2683	TATCTGAAACCAACAGAGACACTTCCCTGAGTGCACAGTCCATTAGAGAAAACTGGA	2742
Db	2676	TGCTCT-----AGAAAAACACTCCCTTTGGACACACAGTCCATAGAGAAAACTGGA	2726
QY	2743	AAAGATTTATGTCTTCAAAAATTTGAGTGGCAGTTCAGAGGACATTTGAGAGACTGGCC	2802
Db	2727	AAAGACATTAAAGTGTCTAGAGACTGATGTCCAGCTGGAGAGACATTTCTTGACAGACTGGCC	2786
QY	2803	AGCATTTTCACTAGGACCTTCTAGTTCAACACAAACAAACAAACAAACAGAGACAACA	2862
Db	2787	GGCGTCTCTGTAGAGACTTCCACACT-----CAACAACAAACAGAAACAACA	2831
QY	2863	AAAGCAATGGTTCAAAACAAAGGCACACCCACAGTCAAGTGTTTAACTCTCTCCCTTTA	2922
Db	2832	AAAGCAACGGTTCAACAAAAAGGCACACCCACAGTCAAGTGTTTAACTCTCTCCCTTTG	2891
QY	2923	TCTCATCTTCCCAATTAATGTTTCCAGGCTTGTCAACCCCTCTCTTCTTACCCACATCT	2982
Db	2892	TC---TCATGCTCAATTAATGTTTCCAGGACACATCAGGCCCTGTGTTCTCTGCCCCGCT	2948
QY	2983	GTAACCACTGGCACACTGCACAGATGTCTTAAGCATAGACTTCAAGGATTCATTCCTCTGC	3042
Db	2949	GTCC-----CAGATATTTTAAAGCACACAGCCCAAGGATTTGTTTCCCTGC	2993
QY	3043	AGATATCTTCTGCATCTCTCAACACACAGCGCAAGTTTCTCTCAATTCACAGAAAC	3102
Db	2994	AAATATCTTCCGATCTCTCTCAACACAGCGCAAGTTTCTCTCAATTCACAGAGAAC	3053
QY	3103	TGTCTGAAAAACAAGACTCAGATTAACCTTTCCCAAGTCTTATCTACGTCAAGACCTTG	3162
Db	3054	TGCTCTCAACACGAGACTCAGACAGCTCTCCCAAGTCTTCACTACATCAAGACCCCA	3113
QY	3163	CCCTCCAGTTAACTACACAGCGCCAAAGCCATGTACACCTCAACCCGAGTAATATACAGTTAA	3222
Db	3114	CCCTCCAGTTAACTACACAGCGCCAAAGCCATCCCGACCCGTTTCCGCGCATATACAGCAAA	3173
QY	3223	CAGGAGATCCCTCAAAAAATAGCATGACACTTGATCTGAACAGTAAAGTTCCAAATGTGAT	3282
Db	3174	CTAAGGAGCGCAAAAAAATAGCATGACACTTGATCTGGCAAGTCTTCCAGGTTGAC	3233
QY	3283	GACACCTTTGGCTGTAGCACCATTAATAGTAATGCTGTTATATCCAGTGCAGACAGACTG	3342
Db	3234	GACAGCTTTGGCGCGCGCAACAGTGTCAACGCCGTATATCCAGGAGACAGACAGACTG	3293
QY	3343	TTTCAACCCAGTAGAGAGAAATGCAGATTAGATGTCAATATACAGACTCAACCTCCAGTTT	3402
Db	3294	TTTCAACGCCGGGAGAGACAGTGTAGTAAAGTGTAAACACCGAGACTCAATCCACAGATC	3353
QY	3403	GAGACCTTCTTGAAGCATATATGCTTCAAGTATGATATCAACAGTAACTTTTAAGTCAGAA	3462
Db	3354	GAGACCTTCTTGAAGCATCATGCTTCAAGTATGATATGATATCAACAGTAACTTTTAAGTCAGAA	3413

OY	3463	GTTCCTGCTCTCTCTCTGAAAAGGCTGAAAATGATGATACCTACAAAAGATGATGTCAT	3522
Db	3414	GTCCCGCTCTCTCTCTCCGAAAAAGGCGGAAAATGACGACACCTCCAAAAGACGTCAT	3473
OY	3523	CATTATCAAAAGTGTCAAAAGGAAGATGGAAAGCTGAAAGAAAGAAAGCTTGTAGCAATGGC	3582
Db	3474	CATTATCAAAAGTGTCAAAAGGAAGATGGAAAGCTGAAAGAAAGAAAGCTTGTAGCAATGGC	3533
OY	3583	ATGGCAATGTGAGGCTCTCAGATGGCCCTCCCATAGTTCCTCAGCTCAGGTGAAAAT	3642
Db	3534	ATGGGATGTGAGGCTCTCAGATGGCCCTCCCATGTCTCCCTCAGCTCAGGTGAAAAT	3593
OY	3643	GGAGAGATATCATCTATTATTCACAGAGATACACGAGACTCTACAGACATACCAA	3702
Db	3594	GGAGAGATATTTATCATCTTTCAGAGGACACACCGAANAACCTTCCAGGACATACCAA	3653
OY	3703	GCAAAACACCGCTATACAGAAAGCACTGAAATGGCTGAAAGGTCAACAGATAGGCTTGA	3782
Db	3654	GCGAAACACCGCTTACACAGAAAGCGCTGATGGCTGAAAAGGCGACAGATAGGCTCGGA	3713
OY	3783	GCATTTCTCTCTGTTATTCAGGCTCAAAATGTGGAACTGGAACCTTATAGCTGTAAA	3822
Db	3714	GCATTTCTCTCTGTTATTCAGAGCAAGAGATGTGGGACTTGAATGGCTGTAAA	3773
OY	3823	CAGGTGACTATGTGACAAAACACATCTTTCAGCAAGAAAGATAGTAAGACACTAAGA	3882
Db	3774	CAGGTGAGTACGTACCAAAAACATCTCTCCGACACAGAGAGATGGTGAAGCGTTGAG	3833
OY	3883	GAAAGATTAAGAAATGATGAGGCCATCTGATCATCCAAACATCATTAAGATGTGGGAGC	3942
Db	3834	GAAAGATCCGAGATGAGGTGTACACTCAACATCAACAAATATCCGAGATCGTGGGGCC	3893
OY	3943	ACGTGTGAGAGAGCAATTTCAATCTCTTCATTGAATGGAGGAGATCGGTGCT	4002
Db	3894	ACGTGTGAGAGAGCACTCAACACTTTCATTGAATGGATGGCGGAGATCTGTGCT	3953
OY	4003	CATTGTCTGACTAAATATGAGAGCCCTCAAAAGATCAGTATTATTACTACCTGAACAG	4062
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OY	4063	TTACTCGGTGGCTTGTGATCTTCATGAAAACCAATATTCACAGAGATGTCAAAGT	4122
Db	4014	TTACTCGGTGGCTTGTCTCTCTCTCCAGAGAACCAATATTCACAGAGAGCTCAAAAGT	4073
OY	4123	GCCATTTGTCTAATTTGACACACTGTGACAGAGCTTAAGATTTGACGATTTGGAGCTCA	4182
Db	4074	GCCAACTGCTCATTTGACAGACACGGCTCAGAGCTTGAATTTGACAGACTTTGGAGCTCT	4133
OY	4183	GCCAGTTGGCATCAAAAGGAAGTGTGACGAGAGTTTCAGGACAATTTACTGGGACA	4242
Db	4134	GCCAGTTGGCATCAAAAGGAACCGGTGACGAGAGTTTCAGGACAAGTTACTGGGACA	4193
OY	4243	ATTGATTTATGGAACCTGAGGATCTTAAGAGGTCAACAGATATGGAAGAGCTGTGATGA	4302
Db	4194	ATTGATTTCAAGGGCGCTGTGAGGTCTTAAGAGGTCAACAGATATGGAAGAGCTGTGATGA	4253
OY	4303	TGAGATGTTGGCTGTCTATTATAGAAAATGGCTGTGCAAAAACCAACATGGAATGCAGA	4362
Db	4254	TGAGATGTTGGCTGTGCTCATTTATAGAAAATGGCTGTGTGCAAAAACCACTTGGAAATGCAGA	4313
OY	4363	AAACATCTCAATCATCTTGGCTTGTGATATTTAAGATTGCTAGTGCAACTACTGCTCATCG	4422
Db	4314	AAACATCTCAATCATCTGCGCTGTGATTTAAGATTGCTAGGGAACAATCTGCAACCTGCG	4373
OY	4423	ATCCCTTACATTTGTCTCTCGGTTTACGAGATGTGGCTCTTGTTGTATAGACTCAA	4482
Db	4374	ATCCCTGTACACCTGTCTCCCGGCTGTGCGGAGAGTGGCGCTGCTGTAGAACTCTAG	4433
OY	4483	CCTGAGCAACACTTCATCAAGAGAGCTACAAACATTCACAGTCTTTCGTAATCTACATGG	4542
Db	4434	CCTGAGGACGGGCTCTCGTCAAGAGAGCTGTGAACAATTCGGGTCTTCGTAACACGTTG	4493
OY	4543	TAGCCAAATTATTCGATCAACTACAGTAGAAACAGAGATCTCAACAGAGAAAAAAACT	4602

Db	4494	TAGTAAATGTTGCAGATCAGCTCTAATGAGAGACAGATATGCAACCGGAGAGAGAAAG	4553
QY	4603	TG-----TGGGAAACCACATGATGATATCTACTGGCCATGATGCCACTGAACAGTATGAC	4568
Db	4554	AGAACTTGTGGGCGCACCATTCCGCTAACGCGACGCCCTTCAGGCACTGAAACAGCCGAGAAC	4613
QY	4659	GAGGCAAGTGGGGAAACCCCTTAACGTAAATGATATGATTTGAACAAATTCATGATCTACTAC	4718
Db	4614	GGGGCCACAGCGGGAA--CCGTAACCTAAAGCATGTGATTTGAACAAATTCATGACTGTATTAAG	4672
QY	4719	CTCAGTATGCA-AAAGCCAAACTAGTGCAGAAACTGTAACTGTGCCCTTCAAGAACT	4777
Db	4673	CTCAGTATGCGAGACATCTACAGTCTGTGCGAGAACTGCACACCGTGCCCTTTCACGAGCT	4732
QY	4778	GGCCCTAGCTGAAACAGGAAACAATGATGTTGTCATGACTAAATTCAGAAAGCATATTT	4837
Db	4733	GGCTCTGGGGACACGAGAAAGCATGTGAGTTTGTCATGATTAAGAAACAGAGCATATATTT	4792
QY	4838	TATTTTTTGGAGCACTTTTTCGCAA	4864
Db	4793	TA--TTTTGGAGCACTTTTTCGCAA	4817

## RESULT 2

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: Sequence 7, Application US/10000864
: Patent No. US20020146798A1
:
: GENERAL INFORMATION:
: APPLICANT: CADUS PHARMACEUTICAL CORPORATION
: TITLE OF INVENTION: HUMAN MEK PROTEIN AND
: TITLE OF INVENTION: AND USES THEREFOR
: FILE REFERENCE: CRI-085C2PC
: CURRENT APPLICATION NUMBER: US/10/000,864
: CURRENT FILING DATE: 2001-10-31
: EARLIER APPLICATION NUMBER: 09/4423,890
: EARLIER FILING DATE: 2000-06-03
: EARLIER APPLICATION NUMBER: PCT/US99/05556
: EARLIER FILING DATE: 1999-03-15
: EARLIER APPLICATION NUMBER: USSN 60/078,153
: EARLIER FILING DATE: 1998-03-16
: EARLIER APPLICATION NUMBER: USSN 60/099,165
: EARLIER FILING DATE: 1998-09-04
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 7
:
: LENGTH: 5253
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (15)..(4493)
: US-10-000-864-7

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Query Match	65.18; Score 3417; DB 12; Length 5253;
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Best Local Similarity 83.5%; Pred. No. 0;  
Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;

QY	1	GAGAAATATGCGGGGCGGGGAAATCGGGCTCGTCCGGGATTCGCCGGGCGCAGG	60
Db	9	GAGAAATATGCGGGGCGGGGCGGGGAAATCGGGCTCGTCCGGGATTCGCCGGGCGC	68
QY	61	GCTACGAGCCCTGAGGCGAGCGCGCGC-----GGAGGAGCCCTCAAGGCGAGAGC	111
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QY	112	GCGCC---GCGGCTGCCCGCGGAGCTCTCGGGAGGCGGGGCGCGCGCGCGAGCGG	168
Db	129	GCGCGCCAGCGGCGCGCGCGGGGCTCTCGGGAGGCTGCGAGCGCGGCGCGCGAGCGC	188
QY	169	GCGGACTGGGGGCGGGGCGGAGCTGCCGAAGTGTGGAGTCTGGACGACAGCTGCT	228
Db	189	GCGGACTGGGGGCGGGGCGGAGCTGCCGAAGTGTGGAGTCTGGACGACAGCTGCTGCG	248

QY	229	GAGCAGCGCGCTCTTCTTGCCGCGCTCACCGCGCGCCCT--CTTCGACTTTCGCCGTGCGG	285
Db	249	GAGCAGCGCGCTTCTCTTGCGCGCGCGCTCGCGCGCCCTGGCCACTACTTCTCCGCTGCGG	308
QY	286	GAGCCCGCGGACGACGAGGGGAGTGGGACCGGGCTCCAGCCTTGCGCGGCGCGCGCC	345
Db	309	GAGCCCGCGGACGGGGCTGCAGGAGGAGTGTGCTTCAGCGCGCGCGGGACCGCCACCC	368
QY	346	CACGAGCGCGGAGCCGCGCGCGCGCCACCTTACGAGTGGTGGCGGCGCGGACAC	405
Db	369	CGGGAGGGGAGTATCGCTGGGCTCCACCTGTCCGAGCTGGCGCGCGCGGGGACAC	428
QY	406	GCGCGCTGAGTCTCCCGACGCGCGCGACCGCGGGAGAGCGGCGCGCGCGCGGCGG	465
Db	429	GCGCGCGGAGCCCCCGGGG-----GGGAGCCG	458
QY	466	TCTCTCGACGCGCGCCCCCGCGCTCGTAGATGGAGATTAAGAACTCTCAAAGGCTTG	525
Db	459	CCCTCTCGACGCGCGCCCCCTCGCGTAGAGATGGAGATTAAGAAACCCCTCAAAGACTG	518
QY	526	CACAAATGAGTATGATCGTCCAGAGCAATGATCAGGAGAAACTGAAAGCACTCT	585
Db	519	CACAAATGAGGAGATCCCGCGAGAGATATCCGGAGAAAGCTCAAGCGACACTGT	578
QY	586	ATCGCAGCGCTGGAACGACAGATGGTTTGAAGAGAGAAATAGCGGAGCGCTGGTGTA	645
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QY	646	AAACCAATCCAGTTAAAGAGATGATCTGAAATGAATCATCTTACAGCTAGTCTCCA	705
Db	639	AAGCCAAATCCCTATTAAAGGAGATGATCTGAAATGAATCAATCTTGGCAGCTAGCGCCAG	698
QY	706	GAGAGGCTCCAGGCAATGCGGCTTCCACAGCTTCCAAAGCGCGAGCGAGTCTCTCT	765
Db	699	GGAAGGGCCAGGCAAGTTCCGCTGCACACGCCCCCAAGGGCCGACGAAGCCACTCTCT	758
QY	766	GCGCACTCCCATCAGGTCCGACAGTGAATCTTCAGAGTAAAGGAGAGAAAGA	825
Db	759	GCGCAGCTCTCCGTAGGGGCGCTCGTGMACCCGGAATCCCGAGAGTAAGACGGAACGA	818
QY	826	GTTTTCCCGACGCTTTTTCAGAGTGGGAGAAATACACACCCCGAGAGCCCTTCTACCA	885
Db	819	GTGTCCCGCGGCTTTTCCAGAGTGGGAGATACACACCCCGAGAGCCCTCATCCG	878
QY	886	GATGCTTCTCACCATATAGCCCTGAGAGAAACAAACCGCGCTTAAACAAAGTGAATGCGG	945
Db	879	GATGCTTCTCCCGCTACAGCCACGAGAGAGACAGCGCGCGGTGAACAAAGTGAATGAGA	938
QY	946	GCGCAGCTGATCTTACGAGAGAGATGAGGCTTAACTTTTCTGATTTGGAGAGACAGC	1005
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QY	1186	AGTAGGCGTAGCTCAAGATCAAAAGCTCACTCTCAACACATCCAGAAAGTTTGTTCAC	1245
Db	1179	AGTAGGCGTAGCTGAGAAATCAAAAGCTCATCCCGGAACACCATCCAGAAAGTTTGTTCAC	1238
QY	1246	CGCATGTCAAAATTCATATACATTTGATCATCTAGTACTTCTAGCTGTAGATTACAGAAAC	1305
Db	1239	CGCATGTCAAAATTCATACACAGCTATATGCTGTAGCACATTCACACTATAGTTCAAGAAAC	1298



[illegible]

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OY 4603 TG--TTGGGGAGAACCAATTGATATTTCTTACATGTGGCCATGTATGTCACGACGACCTATGAAC 4658
Db 4554 ABAACTTGTGGGGCAGACACTGTCGGCTTACCGACGACCTCTACGCGACTGAACACGACGAAAC 4613
OY 4659 GAGGCCAGTGTGGGGAACCCCTTACCTAAGTATGTGATTTGACAAATTCATGATCTGTACTTAAG 4718
Db 4614 GGGGGCAGCGGGGAA--CGGTACTTAAAGCATGTGATTTGACAAATTCATGATCTGTACTTAAG 4672
OY 4719 CTCAGTATGCA--AAAGCCCAACTATGTGACGAAACTGTAACTGTGCTTTGAAGAACT 4777
Db 4673 CTCGATATGCAACACATCTACACGCTGTGCGAGAACTGTGCACACCGTGCCTTTACAGAACT 4732
OY 4778 GGGCCCTAGGTGAACAGGAAACAATGAAGTTTGCAATGACTAAATTTGACAAACATATATT 4837
Db 4733 GGCTCTGGGGGACCAAGAAAGCGCATGTGATTTGTGACTTAAGAACACAGACATTAATT 4792
OY 4838 TATTTTTTTGGAGCACTTTTTTCAGCAA 4864
Db 4793 TA--TTTTTGGAGCACTTTTTTCAGCTA 4817

RESULT 3
US-10-000-864-1
; Sequence 1, Application US/1000864
; Patent No. US20020146798A1
; GENERAL INFORMATION:
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: HUMAN MERK PROTEIN AND NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: CPI-085CPC
; CURRENT APPLICATION NUMBER: US/10/000,864
; CURRENT FILING DATE: 2001-10-31
; EARLIER APPLICATION NUMBER: 09/423,890
; EARLIER FILING DATE: 2000-06-03
; EARLIER APPLICATION NUMBER: PCT/US99/05556
; EARLIER FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: USSN 60/078,153
; EARLIER FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: USSN 60/099,165
; EARLIER FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3911
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(3908)
US-10-000-864-1

Query Match 62.7%; Score 3286.4; DB 12; Length 3911;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 3580; Conservative 0; Mismatches 331; Indels 45; Gaps 5;

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Db 241 CCCACATGCTTTTCAGAGTGGAGATCACACACCCCGCAAGGCCCTTCCACCAATG 300  
QY 890 GCTTCTACCATATATAGCCCTGAGGAAACAAACCCGCTGTTTAAACAAAGTATCGGGCCA 949  
Db 301 GCTTCTACCATATATAGCCCTGAGGAAACAAACCCGCTGTTTAAACAAAGTATCGGGCCA 360  
QY 950 GACTGTACTTACTGACAGATAGGCGCTTAACCTTCTGATTTGAGAGACAGCCAG 1009  
Db 361 GACTGTACTTACTGACAGATAGGCGCTTAACCTTCTGATTTGAGAGACAGCCAG 420  
QY 1010 ACAATAAATACCGGCTTTATTGGGCTTCAGACATGCACTGTGCAACCTTACAGCCAAATG 1069  
Db 421 ACAATAAATACCGGCTTTATTGGGCTTCAGACATGCACTGTGCAACCTTACAGCCAAATG 480  
QY 1070 GATTCATCTGATTTGATGCTCCGGGCTTCACTAGACAGCTTACAGCCAAATG 1129  
Db 481 GATTCATCTGATTTGATGCTCCGGGCTTCACTAGACAGCTTACAGCCAAATG 540  
QY 1130 TATGAGAAAAAATTTTAAAGAAATTTGAGGTGAGAGTTGTTCCAGAAATATCACATA 1189  
Db 541 TATGAGAAAAAATTTTAAAGAAATTTGAGGTGAGAGTTGTTCCAGAAATATCACATA 600  
QY 1190 GGGGTAGCTCAAGATCAACATCTCCATCTGTAACACATCCAGAGTTTGTTCACGCA 1249  
Db 601 GGGGTAGCTCAAGATCAACATCTCCATCTGTAACACATCCAGAGTTTGTTCACGCA 660  
QY 1250 TGTCAATTTCTCATATGTTGTCTCATCTAGTACTTCTACGTTAGTTTGAAGAAACGA 1309  
Db 661 TGTCAATTTCTCATATGTTGTCTCATCTAGTACTTCTACGTTAGTTTGAAGAAACGA 720  
QY 1310 TAAAGATGAGAGAGAACAGATGTCTCTATTTGTTGGGCGATGCTGATGAAGAA 1369  
Db 721 TAAAGATGAGAGAGAACAGATGTCTCTATTTGTTGGGCGATGCTGATGAAGAA 780  
QY 1370 GTCTTACAGTGTGTGAAGAGGCTGACAGAAAGCTGCAACCACTGATGATGATTT 1429  
Db 781 GTCTTACAGTGTGTGAAGAGGCTGACAGAAAGCTGCAACCACTGATGATGATTT 840  
QY 1430 GGGCAGAGAGTGTAGAGAAATAGAGAACTTTAATATGTCCCTTGTAGATCTAATG 1489  
Db 841 GGGCAGAGAGTGTAGAGAAATAGAGAACTTTAATATGTCCCTTGTAGATCTAATG 900  
QY 1490 GGAATCTCATGATTTTCTACAGCCAGAGTGTGCAAGTCTGTGATTCCTTCTTCC 1549  
Db 901 GGAATCTCATGATTTTCTACAGCCAGAGTGTGCAAGTCTGTGATTCCTTCTTCC 960  
QY 1550 TCAGACTGCACAGCAAAACCGTACAGAGAGCGTTTGGGTGATTCACGAAGAATC 1609  
Db 961 TCAGACTGCACAGCAAAACCGTACAGAGAGCGTTTGGGTGATTCACGAAGAATC 1020  
QY 1610 AAGAGAGCAATTTTAACTTACTATTATGAACTCAGCAAAATCCCTCGCTTACAAAG 1669  
Db 1021 AAGAGAGCAATTTTAACTTACTATTATGAACTCAGCAAAATCCCTCGCTTACAAAG 1080  
QY 1670 ATTATGCTGAGCCATGATTCAGGTGTTTGAATGGAATCGTTGGCTGTTATTTCTA 1729  
Db 1081 ATTATGCTGAGCCATGATTCAGGTGTTTGAATGGAATCGTTGGCTGTTATTTCTA 1140  
QY 1730 GAAACGTGGAATGTGAGAGATGGCCCTCAGGGCTTTCCTCCATGATGTAGGGGCC 1789  
Db 1141 GAAACGTGGAATGTGAGAGATGGCCCTCAGGGCTTTCCTCCATGATGTAGGGGCC 1200  
QY 1790 TGTGTTGGCAATTTGGGAGAGCACTGAAATTTCTGGGGGACAGTGAAGAGCCGA 1849  
Db 1201 TGTGTTGGCAATTTGGGAGAGCACTGAAATTTCTGGGGGACAGTGAAGAGCCGA 1260  
QY 1850 GTGGGGAGCCACAGTGGGCTTCCAGACAGATCTCAGAGATGTGTGGAGCAT 1909  
Db 1261 GTGGGGAGCCACAGTGGGCTTCCAGACAGATCTCAGAGATGTGTGGAGCAT 1320  
QY 1910 GGTGAGCGTGTGTCAATGTGTGTGACCCCTGTCTCAAAAGTGTACGTGTGCTT 1969  
|||||

Db 1321 GTGCACTGTCTGTCTATATAGTGTGCGGTGACCCGTGTCTCAAAAGTGTACGTGTGCTT 1380  
QY 1970 TAAAAACATTGAGAGCCATGCTGATATATCTCTTCCACAGTTTGGGAAAGATCA 2029  
Db 1381 TAAAAACATTGAGAGCCATGCTGATATATCTCTTCCACAGTTTGGGAAAGATCA 1440  
QY 2030 AACTTCAGAGACTTCTCAGCCAGTTGTAGACACATCTTACGTAATGTGAGATGCCA 2089  
Db 1441 AACTTCAGAGACTTCTCAGCCAGTTGTAGACACATCTTACGTAATGTGAGATGCCA 1500  
QY 2090 ATAGCCGACAAAGTACAGCTTCCATATCAACACACTGTGGAACCTGTGCAAGGCCAG 2149  
Db 1501 ATAGCCGACAAAGTACAGCTTCCATATCAACACAGTGTGGAACCTGTGCAAGGCCAG 1560  
QY 2150 GAGAGTGGAGAGTTGGAGAGAAATTAAGAGTGAATCCATGTAATGTGAGTGTG 2209  
Db 1561 GAGAGTGGAGAGTTGGAGAGAAATTAAGAGTGAATCCATGTAATGTGAGTGTG 1620  
QY 2210 ATATGTCTTAAATTTGATTTCTTGAACCAACAACTGAATCAAAATTTGCAAGACTTC 2269  
Db 1621 ATATGTCTTAAATTTGATTTCTTGAACCAACAACTGAATCAAAATTTGCAAGACTTC 1680  
QY 2270 TTGGCCGCTTGTCTATATAGATAGACTGTGTTGGAATTTCCGTGATTTATCTC 2329  
Db 1681 TTGGCCGCTTGTCTATATAGATAGACTGTGTTGGAATTTCCGTGATTTATCTC 1740  
QY 2330 ATATGTCTTAAATTTGATTTCTTGAACCAACAACTGAATCAAAATTTGCAAGACTTC 2389  
Db 1741 ATATGTCTTAAATTTGATTTCTTGAACCAACAACTGAATCAAAATTTGCAAGACTTC 1800  
QY 2390 GTTCCCTCTTAACTTTGCTTGGAGTCACTGTAATTTCCACTCAATGTTGGCAAC 2449  
Db 1801 GTTCCCTCTTAACTTTGCTTGGAGTCACTGTAATTTCCACTCAATGTTGGCAAC 1860  
QY 2450 TTTCCAGAAAGATCTACTTATAGTCTCAGAAATGTTACTACAGTACCCATGTGTT 2509  
Db 1861 TTTCCAGAAAGATCTACTTATAGTCTCAGAAATGTTACTACAGTACCCATGTGTT 1920  
QY 2510 CAAAACGTGTAAGAAATGCTAGTGTTCAGATTCCACTTCCACAGAGTGGTGGCC 2569  
Db 1921 CAAAACGTGTAAGAAATGCTAGTGTTCAGATTCCACTTCCACAGAGTGGTGGCC 1980  
QY 2570 GTTGTATGCTATTTGACAGATGAGGTGAAATTTGCCAGGCCATCCAGTTGGGCTAGAG 2629  
Db 1981 GTTGTATGCTATTTGACAGATGAGGTGAAATTTGCCAGGCCATCCAGTTGGGCTAGAG 2040  
QY 2630 ACACTTGGATGGTCAACAGAGACAGCTTCTGCAAGGATCTGTCCCAACATATCTGG 2689  
Db 2041 ACACTTGGATGGTCAACAGAGACAGCTTCTGCAAGGATCTGTCCCAACATATCTGG 2095  
QY 2690 AAACACAGAGACAGTTCCTGAGTGCACAGTCCATTTAGAGAAACTGSAAGAGAT 2749  
Db 2096 AAACACAGAGACAGTTCCTGAGTGCACAGTCCATTTAGAGAAACTGSAAGAGAT 2148  
QY 2750 TATGTCTTACAAAATTTGAGTGCAGATTTCAGAGACATTTCTGAGAGACTGGCCAGATTT 2809  
Db 2149 TATGTCTTACAAAATTTGAGTGCAGATTTCAGAGACATTTCTGAGAGACTGGCCAGATTT 2208  
QY 2810 CAGTAGACCTTCTAGTTCACAAACAAACACACACACACAGAGACAAACGCA 2869  
Db 2209 CAGTAGACCTTCTAGTTCACAAACAAACACACACACAGAGACAAACGCA 2253  
QY 2870 TGTGTTCAAAAG 2929  
Db 2254 TGTGTTCAAAAG 2310  
QY 2930 ATTCCCAATTAATGTTTCAAGCTTGTCAACCCCTTCTTCAACCCATCTGTACAG 2989  
Db 2311 ATTCCCAATTAATGTTTCAAGCTTGTCAACCCCTTCTTCAACCCATCTGTACAG 2367  
QY 2990 CTGGCACTGCAACAGATGTCTTACAGATAGACTTCAAGGATTCATTCCTGCAAGATAC 3049  
Db 2368 CTGGCACTGCAACAGATGTCTTACAGATAGACTTCAAGGATTCATTCCTGCAAGATAC 2415  
-----CAGATATTTCTAAGCAGACAGACCCAGGATTTGTTCCCTGCAAAATAC

QY	3050	CTTCTGCATCTCTCTCAAAACACACAGCGCAAGTTTCTCTACAAATTCACAGAAACTCTCTG	3109
Db	2416	CTTCGGCATCTCTCTCAACACACACAGCGCAAGTTCTCTCTACAAATTCACAGAAACTCTCTG	2475
QY	3110	AAAAACAAGACTCAGATTAATACTTTCCCAAGTCCTTTACTAGTCAAGACCTTGCCCTCCA	3169
Db	2476	AACACCGAGACTCAGACCACTCTCCCAAGTCCTTCACTAGTCAAGACCCCACTCTCCA	2535
QY	3170	GTAACATTCACAGGCCAAAGCCATTAGACTTACCCAGGTAAATCAAGTAACAGGGAG	3229
Db	2536	GTAACATTCACAGGCCAAAGCCATTAGACTTACCCAGGTAAATCAAGTAACAGGGAG	2595
QY	3230	ATCCCTCAAAAAATAGATGACACTTGATGACTGAAAGTGGTTCACAAATGTGATGACACT	3289
Db	2596	ACGCCACAAAAAAGTATGATGACACTTGATGACTGAAAGTGGTTCACAAAGTATGACACACT	2655
QY	3290	TTTGCTGTAGCAGCAATATGATATGATGCTGTTATATCCAGTAGACAGACAGTTCACCC	3349
Db	2656	TTTGCTGTAGCAGCAATATGATATGATGCTGTTATATCCAGTAGACAGACAGTTCACCC	2715
QY	3350	CAGTAGAGAGAAATATGCAATATGATGCTAATATCAGAGTCGAATCCAGTATATGAGGC	3409
Db	2716	CAGTAGAGAGCAATATGCAAGTTATGATGATGACACAGAGTCAATCTCAGACTCAGAGGC	2775
QY	3410	TTTCTTGAGGACTATGCTCCCTTCAAGTATACAAACATTAATTTTAACTCAGAGTTGCTG	3469
Db	2776	TTTCTTGAGGACTATGCTCCCTTCAAGTATACAAACATTAATTTTAACTCAGAGTTGCTG	2835
QY	3470	TTCCGTCTCCCGAAAAAGCGTGAATATGATATCTTACAAATATATGTGATCTATATC	3529
Db	2836	TTCCGTCTCCCGAAAAAGCGTGAATATGATATCTTACAAATATATGTGATCTATATC	2895
QY	3530	AAAAAGTGAAGAGAAAGATGGAAGCTGAAGAAGAAAGAACTTTAGCAATTCAGCATGCGAA	3589
Db	2896	AAAAAGTGAAGAAAGATGGAAGCTGAAGAAGAAAGAACTTTAGCAATTCAGCATGCGGA	2955
QY	3590	TGTCAAGGCTCTCAGGATGCCCTCCCATATGTTCTCAGCTGAGGTTGAAAAATGAGAG	3649
Db	2956	TGTCAAGGCTCTCAGGATGCCCTCCCATATGTTCTCAGCTGAGGTTGAAAAATGAGAG	3015
QY	3650	ATATCATCATTTATTCACAGAGTATACACAGAGACCTTACAGAGCATTCACAAAGCAAAAC	3709
Db	3016	ATATCATCATTTATTCACAGAGTATACACAGAGACCTTACAGAGCATTCACAAAGCAAAAC	3075
QY	3710	AACCGTATAGAGAAACACTGAATGGCTGAAGAAGTCAACAGATAGGCCCTTGAGACATTTT	3769
Db	3076	AGCCTTATACAGAAAGACGCTGAGCTGCTGAAGAAGCCAGACAGATAGGCCCTTGAGACATTTT	3135
QY	3770	CTTCTGTATTCAGGCTCAAGATGTGGGAATCGGAACCTTAATGGCTTTTAAACAGTGA	3829
Db	3136	CTTCTGTATTCAGGCTCAAGATGTGGGAATCGGAACCTTAATGGCTTTTAAACAGTGA	3195
QY	3830	CTTATGTCAGAAACACATCTCTTCAGACCAAGAAGAGTAGTAGAACACATAGAGAGACGA	3889
Db	3196	CTTATGTCAGAAACACATCTCTTCAGACCAAGAAGAGTAGTAGAACACATAGAGAGACGA	3255
QY	3890	TAAACAATGATGAGCCATCTGTAATCATTCACCAACATCATTTAGATGTGGGAGCCAGTGTG	3949
Db	3256	TAAACAATGATGAGCCATCTGTAATCATTCACCAACATCATTTAGATGTGGGAGCCAGTGTG	3315
QY	3950	AGAGAGCAATTTACAAATCTCTTCATTTGATGATGAGTGGCAGGGGATCGGTGTCAATTTGC	4009
Db	3316	AGAGAGCAATTTACAAATCTCTTCATTTGATGATGAGTGGCAGGGGATCGGTGTCAATTTGC	3375
QY	4010	TGAGTAATATGAGCCCTTCAAAAGATCAGTATGTTAACTACACTGAACAGTTACTCC	4069
Db	3376	TGAGTAATATGAGCCCTTCAAAAGATCAGTATGTTAACTACACTGAACAGTTACTCC	3435
QY	4070	GTTGGCCTTGTGTATTCACATGAAGAACCAATCATTCACAGAGATGTCAAAAGTGCATTT	4129
Db	3436	GTTGGCCTTGTGTATTCACATGAAGAACCAATCATTCACAGAGATGTCAAAAGTGCATTT	3495

OY	4130	TGCTAATTTGACAGCAGCTGGCTCAGAGACTAAGATTTCACATTTTGGAGCTGCAGCAGGT	4189
Db	3486	TGCTCATTTGACAGCAGCCGGTCAGGGCTGAAATTCACACTTTGGAGCTGCAGCAGGT	3555
OY	4190	TGGCATCAAAAGAAAGTGGTCAGAGAGATTTTCAGGACAAATTACTGGGGACAAATTGCAT	4249
Db	3556	TGGCATCAAAAGAAAGTGGTCAGAGAGATTTTCAGGACAAATTACTGGGGACAAATTGCAT	3615
OY	4250	TTATGGCACTGAGGCTCTAAGAGGTCACACGTATGGAAAGAGCTGTATGAGAGTG	4309
Db	3616	TCAATGGGCGCTGAGGCTCTAAGAGGTCAGAGATATGGTGGAGAGCTGTATGATGAGAGTG	3675
OY	4310	TTGGCTGGGATATATATGAATATGGCTTTGGCCAAACACACATGAGATGAGAGAAAAAGCT	4369
Db	3676	TTGGCTGGGCAATTATATGAATATGGCTTTGGCCAAACACACCTTGGATGCGAGAAAAAGCT	3735
OY	4370	CCAAATCATCTTGGCTTTATATATTTAAGATTGGCTATGCAACTCTGCTCATGATCCCTT	4429
Db	3736	CCAAATCATCTGCGCTTATATATTTAAGATTGGCTATGCGCAACTCTGCACTGCTCATGATCCCTT	3795
OY	4430	CACATTTGTCTCTGGTTTACGAGATGTGGCTCTTGTTTGAATCTCAACTCAGG	4489
Db	3796	CACACTGTCTCCCTGGTTTACGAGATGTGGCTCTTGTTTGAATCTCAACTCAGCTCAGG	3855
OY	4490	ACAGACCCCATCAGAGAGACTCTCAAGATCCACTTTGGTACTCATAGGTAG	4545
Db	3856	ACCGGCTCTCGTCAAGAGACTCTCAAGATCCCGGTCTTCGTCACACGTGGTAG	3911

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RESULT 4
US-09-856-754-1
Sequence 1, Application US/09856754
Patent No. US20020055130A1
GENERAL INFORMATION:
APPLICANT: Johnson, Gacy L.
TITLE OF INVENTION: METHOD AND PRODUCT FOR
FILE REFERENCE: CPT 042
CURRENT APPLICATION NUMBER: US/09/856,754
PENDING FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/023,130
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/039,740
PRIOR FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3260
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (486)..(2501)
US-09-858-754-1

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Query Match	37.3%	Score	1955.6	TB	10	Length	3260
Best Local Similarity	82.7%	Pred.	No. 0				
Matches 2376		Conservative	0	Mismatches	444	Indels	54
						Gaps	10

[illegible]











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1485 GACCAACTGGAACTGGGAGCTGCTTGGCCAGAGAGCTTTGGTAGGCTTACTCTG 1544
QY 3786 TCAAGATGGGAGACTGGAACCTTTATGCGCTTTAAACAGTGACTATGTGAGAAACAC 3845
Db 1545 CTATGATGTGTAACCGGAAAGAGAGCTGCTTTAAGCAAGTTCAAGCTTAACCCCTGAG 1604
QY 3846 ATCTTGTGAGCAAGAAAGATGTAAGACACTAAGAGAAAGATTAAGATGAGCCCA 3905
Db 1605 CCCAGAGACCAAGCAAGGAAATGCACTTGAAGTGAATTCAGTTGTAAGAAACCTT 1664
QY 3906 TCTGATCATCTCCAA-ACATCATTAGAGTGTGGAGCCACGTTGAGAAAGCAATTACA 3964
Db 1665 GTTGATGAGCCAAATTTGTCAGTATTTATGCTGTTGAGGAGATCCCTCAGAGAAACACT 1724
QY 3965 ATC--TCTTCAATTGAATGGATGGCAGGGGATCGGTGCTCATTTGCTGAGTAATATG 4022
Db 1725 TTCCATCTTTATGAGCTCTCGCAGGGGGTTCAATTAAGAACCACTAAAGCCTAGG 1784
QY 4023 ACCCTTCAAAAGATCAGTGTATTATTAACACTGAAACGTTACTCGCTGCTTTCGA 4082
Db 1785 AACTCTTACTGAGAACGTGACGAGAACTACACCCGTCAGATTCTGAGGGGCTCCATT 1844
QY 4083 TCTCCATGAAACCAATCATTCACAGAGATGTCAAAGGTGCAATTTGCTAATTGACAG 4142
Db 1845 TTTCATTAATTAATGATTTGCTCATAGAGATATCAAGAGACAAATATCTTAAGGATTC 1904
QY 4143 CACTGTCAGAGACTAAGATTTGCAAGATTTTGGAGCTGCAGCAGGTTGGCATCAAAAG 4202
Db 1905 CACAGGCAATATC--AAGTAGAGACTTTGGGGCTAGTAAGAGGCTTCAGACCATCTGT 1962
QY 4203 AACTGTGAGAGAGCTTCAGGACCAATTAAGTGGGACAAATGCAATTTATGACCCTGA 4262
Db 1963 CTCTCAGACGACAGGAT---GAAGTCTGTCACAGGACGCACTACTGATGATGCTTA 2018
QY 4263 GGTAAGAGGCAACACTATGAGAGAGAGCTGTGATGTAGAGTGGCTGCTGCTAAT 4322
Db 2019 GGTTCATCAGTGAAGAGCTATGAGAGAAAGACAGACATCTGAGTGTAGCATGTACTGT 2078
QY 4323 TATAGAAATGCTGTGCAAAACCAACCATGGAATGCA 4359
Db 2079 GGTAAGAAATGCTACTGAAAGACCAACCTTGGGCTGAA 2115

RESULT 9
US-10-000-864-3
; Sequence 3, Application US/10000864
; Patent No. US20020146798A1
; GENERAL INFORMATION:
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: HUMAN MEK1 PROTEIN AND NUCLEIC ACID MOLECULES
; FILE REFERENCE: CPT-085CPC
; CURRENT APPLICATION NUMBER: US/10/000,864
; EARLIER FILING DATE: 2001-10-31
; EARLIER APPLICATION NUMBER: 09/423,890
; EARLIER FILING DATE: 2000-06-03
; EARLIER APPLICATION NUMBER: PCT/US99/05556
; EARLIER FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: USSN 60/078,153
; EARLIER FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: USSN 60/099,165
; EARLIER FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (124)..(1980)
US-10-000-864-3
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Query Match 1.3%; Score 70.4; DB 12; Length 2013;
Best Local Similarity 47.9%; Pred. No. 2.4e-07;
Matches 327; Conservative 0; Mismatches 346; Indels 9; Gaps 4;

QY 3681 GACCTACAGAGCATATACCAAGCAAAACACCGTTATAGAGAAACACTGATGCTGAA 3740
Db 1137 GACTGTACACAGCAATACGACCACCATGCGTTACCTGACCTCGGACCACTGAGACT 1196
QY 3741 AGTCACAGATAGAGCTTGGAGCAATTTCTTTATGATGAGGCTCAAGATGTGGGAAC 3800
Db 1197 GGGCAAGCTGCTTGGCAAGAGAGATTTTGGTGGGCTCTACCTGTATGATGTGATAC 1256
QY 3801 TGGCACTTAATGCTGTTAAACAGTACTTATGTACAAACACATCTTGTGACAGAGA 3860
Db 1257 CGAAGAGAGCTGCGCTGTTAAGCAAGTTCAGTTAACTCTGAGAGCCACAGACGAA 1316
QY 3861 AGAAGTAGTAAGACACTAAGAAAGATTAAGATTAAGATGAGACCATCTAATCATCA 3919
Db 1317 GGAAGTAATAGCACTTGAGTGTGAATTCAGTTGTGAAAACTTGTTCATGAGCGAAT 1376
QY 3920 ACATCATTAAGATGTTGGAGCCACGTTGAGAGAGCAATTAACAATC--TCTCATTTGA 3977
Db 1377 TGTGATGATTAATGCTGTTTGAAGGATCTCAGAGAAACACTTTCATCTTTATGGA 1436
QY 3978 ATGATGACAGGGGATCGGTGCTCATTTGCTGAGTAATATGAGCCTTCAAGAAATC 4037
Db 1437 GTATATGCCAGGGGTTCAATTAAGAGCACTAAAGCCTACGAGGCTTACTAGAGAA 1496
QY 4038 AGTATTAATTAACACTGAAACAGTACTCCGTGGCTTGTGATATCTCCATGAAACCA 4097
Db 1497 CGTGACGAGAAAGTACCCGTCGATTTGAGAGGGGTCATTTATTCAGATGATTAAT 1556
QY 4098 AATCATTCACAGAGATGTCAAAGGTGCCAATTTGCTAATTTGACAGACGTCGACAGACT 4157
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QY 4158 AAGATTCGAGATTTTGGAGCTGACAGCAGGTGGCATCAAAAGAACTGGTGCAGAGGA 4217
Db 1615 AAGTTAGAGACTTTGGGGCTGATGAACCGCTTACAGACCATCTGCTCTCAGGACAGGA 1674
QY 4218 GTTTCAGGACAAATTAAGTGGGACCAATTCATTTATGAGACCTGAGAGTCTAAGAGTCA 4277
Db 1675 AT---GAAGTGTACAGGACCGCATACGTGAGTGAAGTCTGATATGAGATGAGTGA 1730
QY 4278 ACAGTATGAGAGAGCTGTGATGATGAGTGTGGCTGCTGATTAATGAAATGGCTTG 4337
Db 1731 AGGCTATGGAAGAAAGACACATCTGAGGTGATGATGATGATGATGATGATGATGAT 1790
QY 4338 TGCAAAACCAACATGGAATGCA 4359
Db 1791 TGAAAAGCCACCTTGGGCTGAA 1812

RESULT 10
US-09-967-624-1
; Sequence 1, Application US/09967624
; Patent No. US20020142325A1
; GENERAL INFORMATION:
; APPLICANT: Liao, X. Charlene
; APPLICANT: Chu, Peter
; APPLICANT: Pardo, Jorge
; APPLICANT: Li, Congfeng
; APPLICANT: Zhao, Haoran
; APPLICANT: Wu, Jun
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: PAK2 Modulators of Lymphocyte Activation
; FILE REFERENCE: 021044-000700US
; CURRENT APPLICATION NUMBER: US/09/967,624
; EARLIER FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/280,647
; NUMBER OF SEQ ID NOS: 19
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;; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides, &  
;; FILE OF INVENTION: Antibodies  
;; FILE REFERENCE: PTO20P1  
;; CURRENT APPLICATION NUMBER: US/09/836,392  
;; CURRENT FILING DATE: 2001-04-18  
;; PRIOR APPLICATION NUMBER: PCT/US00/28066  
;; PRIOR FILING DATE: 2000-10-11  
;; PRIOR APPLICATION NUMBER: 60/159,542  
;; PRIOR FILING DATE: 1999-10-15  
;; PRIOR APPLICATION NUMBER: 60/165,914  
;; PRIOR FILING DATE: 1999-11-17  
;; PRIOR APPLICATION NUMBER: 60/189,027  
;; PRIOR FILING DATE: 2000-03-14  
;; NUMBER OF SEQ ID NOS: 34  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 2380  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-836-392-5

Query Match 1.3%; Score 65.6; DB 9; Length 2380;  
Best Local Similarity 51.5%; Pred. No. 4.3e-06;

Matches 202; Conservative 0; Mismatches 184; Indels 6; Gaps 2;

QY 3968 TCTTCAATGATGATGCGAGGGGATCGGCTCATTTGCTGAGTAATATGAGCCT 4027  
DB 175 TATTTATGGAATATATGCGAGGGGCTTCATTTAAGACCAATTAAGCATATGCGCTC 234  
QY 4028 TCAAGAAATCACTACTTATTAATCACTGACAGAGTTACTCGGCTTGGCTATCTCC 4087  
DB 235 TTACTGAGAACTGACTGAGGAATATACCCGTCAGATTTGAGAGGTGTCATTTATTTGC 294  
QY 4088 ATGAAGCAATATCATTCACAGAGATGTCAGAGTGCCTAATTTGCTAATTTGACAGACTG 4147  
DB 295 ACAGTAATATGATTTGCTATAGATATCAAGAGGCGCAATATTCGCGAGTTCAACAG 354  
QY 4148 GTCAAGAGCTAAGATTTGCAATTTTGGAGCTGACGCCAGGTTGGCATCAAAAGCACTG 4207  
DB 355 G---CAAGCTCAAACTAGAGATTTTGGGGCCAGCAAGGCTTCAGACCATCTGCTCT 411  
QY 4208 GTGCAAGAGATTTTCAGGAGCAATTAATCAATTTGCAATTTGCAACCTGATTC 4267  
DB 412 CAGGACAGAGATGAACTGCTG---TCACGGGACACACCATCTGATGAGCCCTGAAGTCA 468  
QY 4268 TAAGAGGTCACAGATGAGAGAGCTGTGATGTATGAGTGTGGCTGTCTATTATAG 4327  
DB 469 TCAGTGCAGAAAGCTATGAGAGAAAGAGACATCTGAGTGTGCATGTACTGTGTAG 528  
QY 4328 AATGGCTTTGCCAAACCAACCATGGAATGCA 4359  
DB 529 AATGCTAATGTAAGGCGCTTGGGCTGAA 560

## RESULT 13

US-10-000-864-5  
; Sequence 5, Application US/10000864  
; Patent No. US20020146798A1  
; GENERAL INFORMATION:  
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION  
; TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: CPT-085CPC  
; CURRENT APPLICATION NUMBER: US/10/000,864  
; CURRENT FILING DATE: 2001-10-31  
; EARLIER APPLICATION NUMBER: 09/423,890  
; EARLIER FILING DATE: 2000-06-03  
; EARLIER APPLICATION NUMBER: PCT/US99/05556  
; EARLIER FILING DATE: 1999-03-15  
; EARLIER APPLICATION NUMBER: USSN 60/078,153  
; EARLIER FILING DATE: 1998-03-16  
; EARLIER APPLICATION NUMBER: USSN 60/099,165  
; EARLIER FILING DATE: 1998-09-04

;; NUMBER OF SEQ ID NOS: 38  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 1935  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(1902)  
US-10-000-864-5

Query Match 1.2%; Score 64.6; DB 12; Length 1935;  
Best Local Similarity 52.6%; Pred. No. 6.7e-06;

Matches 211; Conservative 0; Mismatches 184; Indels 6; Gaps 3;

QY 3953 AGAGCAATTAATCTCTTCAATGATGATGCGAGGGGATCGGTGCTCATTTGCTGA 4012  
DB 1331 AGAAGATCTCTACCATCTTTATGAGATATATCCAGGGGGCTCTGTAAGACCACTTGA 1390  
QY 4013 GTAATATGAGACCTTCAAGAAATGATGATTTAATTAATCACTGACAGATTAATCCGTC 4072  
DB 1391 AGGCTTACGAGCTCTGACAGAGAGTGTACCCGCAAGTACACCCGAGATTCTGAGAG 1450  
QY 4073 GCCTTTGATCTCCATGAAACCAATTCATTCACAGAGATGTCAAAGTCCCATTTGC 4132  
DB 1451 GCATGCTAATCTGACAGACCAATGATTTGTCATCGGACATCAAGGAGCAATATTC 1510  
QY 4133 TAATGACAGACCTGTCAGACTAAGAAATTTGAGCTGACGACGAGGTTGG 4192  
DB 1511 TCCGAGACTCAGCTGG---GAATGGAAGCTTTGGGGT---CAGCAACACT 1565  
QY 4193 CATCAAAAGAACTGTGAGAGAGATTTGACGAGCAATTAATTTGAGGACATTTGA 4252  
DB 1566 ACAGACCATCTCATGATGAGGAGGAGGATTCGCTCTGCTGACTGAC -ACACCTACTGGA 1624  
QY 4253 TGGACCTGAGTACTAAGAGGTCAACAGTATGAAAGAGCTGTGATGATGAGTGTG 4312  
DB 1625 TGAATCTGAACTCATCACTGAGGAGGCTATGAGAAAGGAGCAGAGCTGTGAGCTGG 1684  
QY 4313 GCTGTCTATTATGAATATGCTTGTGCAAAACCACTATG 4353  
DB 1685 GCTGTACTGTGTGATGATGCTGACAGAGAAACCACTTGG 1725

## RESULT 14

US-09-976-740-48  
; Sequence 48, Application US/09976740  
; Publication No. US20020194633A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Arjona, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
; TITLE OF INVENTION: ATHEROSCLEROSIS  
; FILE REFERENCE: 10797-004001  
; CURRENT APPLICATION NUMBER: US/09/976,740  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 09/616,289  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/979,608  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: US 60/031,930  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 60/048,547  
; PRIOR FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 2561  
; TYPE: DNA  
; ORGANISM: Oryctolagus cuniculus

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (246)...(1895)
US-09-976-740-48

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Query Match	1.2%	Score 62.2;	DB 9;	Length 2561;
Best Local Similarity	49.7%;	Pred. No. 3.2e-05;		
Matches 215; Conservative	0;	Mismatches 213;	Indels 5;	Gaps 2

[illegible]

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US-RESULT 15
US-10-023-529-48
: Sequence 48, Application US/10023529
: Patent No. US20020129386A1
: GENERAL INFORMATION:
:   APPLICANT: Lees, Ann M.
:   APPLICANT: Lees, Robert S.
:   APPLICANT: Law, Simon W.
:   APPLICANT: Arjona, Anibal A.
:   TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
:   TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
:   TITLE OF INVENTION: ARTERIOSCLEROSIS
:   FILE REFERENCE: 10797-004001
:   CURRENT APPLICATION NUMBER: US/10/023,529
:   PRIOR FILING DATE: 2001-12-17
:   PRIOR APPLICATION NUMBER: 09/616,289
:   PRIOR FILING DATE: 2000-07-14
:   PRIOR APPLICATION NUMBER: US 09/517,849
:   PRIOR FILING DATE: 2000-03-02
:   PRIOR APPLICATION NUMBER: US 08/979,608
:   PRIOR FILING DATE: 1997-11-26
:   PRIOR APPLICATION NUMBER: US 60/031,930
:   PRIOR FILING DATE: 1996-11-27
:   PRIOR APPLICATION NUMBER: US 60/048,547
:   PRIOR FILING DATE: 1997-06-03
:   NUMBER OF SEQ ID NOS: 53
:   SOFTWARE: FastSeq for Windows Version 4.0
:   SEQ ID NO 48
:   LENGTH: 2561
:   TYPE: DNA
:   ORGANISM: Oryctolagus cuniculus

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (246)...(1895)
;
US-10-023-529-48

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Query Match	1.28;	Score 62.2;	DB 12;	Length 2561;
Best Local Similarity	49.78;	Pred. No. 3.2e-05;		
Matches 215; Conservative	0;	Mismatches 213;	Indels 5;	Gaps 2;

OY	49	CCGGGGCCCAAGGGGCTTACGATCCCTGAGAGCAGAGGCGGGGAGAGACCCCTCAAGGCTGAGC	108
Db	589	CCCCCCCCGGGGGGGCCCCGGCGCCGGCCGGCCGGCCGACGCCCCCGCCCGCCCGCC	648
OY	109	AGCGCGCCCGCCGGGCTGCGCGCGGAGACTCTGTCGGGAGCGGAGCGGAGCGGGGGCCGCGAGCG	168
Db	649	CGCCCGCGCCCGTGTGACCGCGCGCGCGCCCGGCCCGGGGCGCCCCCGGGGGCGCGCGCG	708
OY	169	GCGGACTGGGGGGGGGGCGGGCAGCTGCGCAAAATGTCGGAGTGTGGAGCTGGACAGTGGCT	228
Db	709	CCGGTCGGCGGCACAGCCCCCCCCCTCTGCGCGCGGCC --- GCGCACACCGGGGCCCCCGCGCG	764
OY	229	GAGCAGCGCGGCTCTCTCTCTCTGCGGCTACCGCGCGGCGCTCTCTGACTCTCCCGTCCGCGCGAG	288
Db	765	CAGGGGGCCCGCGCCCTGTGGCGCGCGCGCGCGCGCGCGCGCGCTCCCGCGCGGCGGCG	824
OY	289	CCCGCGGACGACGCGGGGAGTGGGACCGCGCTTCGACGCTGTGGCGGATGCGCGCGCCAC	348
Db	825	CCCCCGGCGCGGCG	883
OY	349	GGAGCCGCCGAGCCCGCGCGCGCGCGCCGACCTTACCGGATCGGTGGCGCGCGCGGACAGCGCG	408
Db	884	GCGCCGTCCCGCGCGCGCCACACGCGCGCGCGCGCGCCACAGCAGCAGCAACACCCCGCC	943
OY	409	GCTCTGATGTCGCCGACGCGGCGCGGAGCGGAGGAGGAGGAGGAGGCGCGCGCGCTGCT	468
Db	944	GCCACGCGCGCGCGGAGGACGACACAGCGCGCGCGCGGAGGGGGGGCGGCGCGCGCGCGG	1003
OY	469	CCTGACGAGGCGCC	481
Db	1004	CCCGCGCGCGCGCC	1016

Search completed: December 28, 2002, 01:13:49  
Job time : 335 secs





## FEATURES

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SOURCE	1..836
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="NT2RP3004289"
	/clone_1id="NT2RP3"
	/cell_type="teratocarcinoma"
	/cell_line="NT2"
	/note=Vector: pWE1BSFL3: mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT	263 a 169 c 180 g 220 t 4 others
ORIGIN	

Query Match	15.0%;	Score 787.8;	DB 9,	Length 836;
Best Local Similarity	98.3%;	Pred. No. 3e-158;		
Matches	825;	Conservative	0;	Mismatches 11;
				Indels 3;
				Gaps 3

QY	4011	GATTAATATGAGCCCTTAAAGAAATCACTAGTTTAACTCACTGAAACAGTTACCTCG	4070
Db	1	GAGTAAATATGAGACCTTTCAAAGATCACTAGTTATTAACCTCACTGAACAGTTACTCG	60
QY	4071	TGSCCTTTCGTATCTCCATGAAAAACCAATCATTCACAGAGATGTCAAAAGTGCCCAATT	4130
Db	61	TGSCCTTTCGTATCTCCATGAAAAACCAATCATTCACAGAGATGTCAAAAGTGCCCAATT	120
QY	4131	GCATATTCACACACCTGCTGACAGACTTAAGAAATTGCAAGTTTGGAGCTGCAGCCAGTT	4190
Db	121	GCATATTCACACACCTGCTGACAGACTTAAGAAATTGCAAGTTTGGAGCTGCAGCCAGTT	180
QY	4191	GGCATCAAAAGAACTGCTGACAGAGACTTTCAGGAGCAATTCAGGGGACAAATTCGACT	4250
Db	181	GGCATCAAAAGAACTGCTGACAGAGAGTTTCAGGAGCAATTCAGGGGACAAATTCGACT	240
QY	4251	TATGGCACTGAGAGTCTAAGAGGTCAACAGATATGAGAGAGAGCTGTATGTAGAGTGT	4310
Db	241	TATGGCACTGAGAGTCTAAGAGGTCAACAGATATGAGAGAGAGCTGTATGTAGAGTGT	300
QY	4311	TGCGTGTGCTATTAATGAAGTGGCTGTGTCAAACACCATGGATGGAGAAAAACATC	4370
Db	301	TGCGTGTGCTATTAATGAAGTGGCTGTGTCAAACACCATGGATGGAGAAAAACATC	360
QY	4371	CAATCATCTTGTGATATTTAAGAATTGCTAGTCAACTACTGCTCCATGATCCCTTC	4430
Db	361	CAATCATCTTGTGATATTTAAGAATTGCTAGTCAACTACTGCTCCATGATCCCTTC	420
QY	4431	ACATTTGTCTCCCGGTTTACGAGATGTGGCTCTTGTTGTTTGAACCTTCAACTCAGGA	4490
Db	421	ACATTTGTCTCCCGGTTTACGAGATGTGGCTCTTGTTGTTTGAACCTTCAACTCAGGA	480
QY	4491	CACACCTTCATCAAGAGACTACTGAAGCATCCAGTCTTCTACTACATGGTAGCCAAAT	4550
Db	481	CACACCTTCATCAANAGACTACTGAAGCATCCAGTCTTCTACTACATGGTAGCCAAAT	540
QY	4551	TATGCAAGATCAACTACAGTAGAAAAACAGATGCTCAACAAGAGAAAAAAACTTGTGGGA	4610
Db	541	TATGCAAGATCAACTACAGTAGAAAAACAGATGCTCAACAAGAGAAAAAAACTTGTGGGA	600
QY	4611	ACCAACATGATATTCTTACTGGCCATGATATCCACTGAACAGCTATATAACAGAGCCAGTGG	4670
Db	601	ACCAACATGATATTCTTACTGGCCATGATATCCACTGAACAGCTATATAACAGAGCCAGTGG	660
QY	4671	GAAACCTTACCTAAGATGTGATGTGACAAATATATATGTCTGT-CTTAACTCAATGTGCA	4730
Db	661	GAAACCTTACCTAAGATGTGATGTGACAAATATATATGTCTGT-CTTAACTCAATGTGCA	719
QY	4731	AAGCCCAAACTAGTGAGAAACGTAAACTGTGCTTTCAAGAAAGTGGCCCTAGGTGAA	4790
Db	720	AAGCCCAAACTAGTGAGAG- AACTGTAAACTGTGCTTTCAAGAAAGTGGCCCTAGGTGAA	778
QY	4791	CAGGAAACACATGAATTTGCTGATGACTAAATTGGCAGAAAGCATAAATTTTATTTTGGGA	4849
Db	779	CAGG- AAACCATGAATTTTNCATGACTAAATTTGGCAGAAACCCATTAATTTTATTTTGGGA	836

## RESULT 2

LOCUS	BM928438	1043 bp	mRNA	linear	EST 12-MAR-2002
DEFINITION	AGENCOURT-66599830 NIH_MGC_121 Homo sapiens cDNA IMAGE:5770238				
ACCESSION	BM928438	5', mRNA sequence.			
VERSION	BM928438.1	GI:19378817	EST.		
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 1043)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

## FEATURES

Plate: LLAM12832 row: p column: 15  
High quality sequence stop: 625.

BASE COUNT	318 a	187 c	190 g	348 t
ORIGIN				
Query Match	13.0%	Score 682.4;	DB 14;	Length 1043;
Best Local Similarity	99.0%;	Pred. NO. 1.2e-135;		
Matches 697; Conservative	0;	Mismatches 6;	Indels 1;	Gaps 1;

QY	4541	GGTAGCAATATTATGACAGTATCACTACAGTGAACAAGATGCTCAACAGAGAAAAA	4600
Db	1	GGTAGCAATATTATGACAGTATCACTACAGTGAACAAGATGCTCAACAGAGAAAAA	60
QY	4601	CTT-GTGGGAGACCACTATGATATTCTACTGCCATGATGCCACTGAGACGTATGAGC	4655
Db	61	CTTGGTGGGAGACCACTATGATATTCTACTGGGCAATGATGCCACTGAGACGTATGAGC	120
QY	4660	AGGCGAGTGGGAGACCCCTTACCTAATGATGTGATGTATACAAATCATGATCCATACG	4711
Db	121	AGGCGAGTGGGAGACCCCTTACCTAATGATGTGATGTATACAAATCATGATCCATACG	180
QY	4720	TCAATATGCAAAAGCCCAACTAGTGCAGAACTGTAACTGTGCCTTCAAGAACTGG	4777
Db	181	TCAATATGCAAAAGCCCAACTAGTGCAGAACTGTAACTGTGCCTTCAAGAACTGG	240
QY	4780	CCCTAGGTGAACAGGAAAAAATGAAGTTTGCATGACTAAATTGGCAAGAGCAATATTTTA	4833
Db	241	CCCTAGGTGAACAGGAAAAAATGAAGTTTGCATGACTAAATTGGCAAGAGCAATATTTTA	300
QY	4840	TTTTTTTTGAGACCTTTTTCAGCAATATTAGCGCGTGAAGGGGCTTCAGGATCTAATTTTAAT	4891



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Db 301 TTTTGGAGCACTTTTCGCAATATTTAGCGCTGAGGGCTCAGAGCTTATTTTAT 360
QY 4900 ATTTCAATTTATTTTCATTTTCATATAGTGATCAACAAGCAGGGGCTTGCATTTCCGT 4959
Db 361 ATTCAATTTATTTTCATTTTCATATAGTGATCAACAAGCAGGGGCTTGCATTTCCGT 420
QY 4960 CAAATTTTGTCTGCTGCTATTAATCAGTATCTGCTCTTTTAAAGTCAGATAGCTA 5019
Db 421 CAAATTTTGTCTGCTGCTATTAATCAGTATCTGCTCTTTTAAAGTCAGATAGCTA 480
QY 5020 TGAGTACCAATACATATATTTTAAAGTGTATCTCTTATAGCCACAGTTGA 5079
Db 481 TGAGTACCAATACATATATTTTAAAGTGTATCTCTTATAGCCACAGTTGA 540
QY 5080 CTTTATTTTCTTAAATACAGGCGAGTGTGCTCATTTGCAATTTTACTGTTGCCCA 5139
Db 541 CTTTATTTTCTTAAATACAGGCGAGTGTGCTCATTTGCAATTTTACTGTTGCCCA 600
QY 5140 TTCAATTTGCTTTTGGAAATATAGTGTGTATTTTCATTTTATTTACATTTTGTG 5199
Db 601 TTCAATTTGCTTTTGGAAATATAGTGTGTGTATTTTCATTTTATTTACATTTTGTG 660
QY 5200 TTTATTCAGGGAAGCTGATCTTTTTCACACCAAAAAA 5243
Db 661 TTTATTCAGGGAAGCTGATCTTTTTCACACCAAAAAA 704

RESULT 3
AL042445 653 bp mRNA linear EST 29-FEB-2000
LOCUS DKEP434D2221.F1 434 (synonym: htes3) Homo sapiens cDNA clone
DEFINITION DKEP434D2221 5', mRNA sequence.
ACCESSION AL042445
VERSION AL042445.1 GI:5421814
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 653)
AUTHORS Blum H., Bauersachs S., Mewes H.W., Gassenhuber J. and Wiemann S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Blum H
MIPS
Am Kioferpitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No al sequence available.
This clone (DKEP434D2221) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
location/Qualifiers
1. 653
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/db_xref="taxon:9606"
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/dev_stage="adult"
/lab host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 199 a 121 c 157 g 173 t 3 others
ORIGIN
Query Match 11.4%; Score 598; DB 9; Length 653;
Best Local Similarity 98.6%; Pred. No. 1,5e-117;
Matches 624; Conservative 0; Mismatches 6; Indels 3; Gaps 2;
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QY 3856 CAGAGCAAGTAGTAGAAGCACTAAGAGAGATTAAGATGATGAGCCATCTGATCAT 3915
Db 1 CAGAGCAAGTAGTAGAAGCACTAAGAGAGATTAAGATGATGAGCCATCTGATCAT 60
QY 3916 CCAAAACATATTAGATGCTGGGAGCCACGCTGTGAGAGACCAATTAACATCTCTCAT 3975
Db 61 CCAAAACATATTAGATGCTGGGAGCCACGCTGTGAGAGACCAATTAACATCTCTCAT 120
QY 3976 GAATGATGAGGAGGAGATGCGTGCATTTGCTGAGATTAATAGAGCCCTTCAAGAA 4035
Db 121 GAATGATGAGGAGGAGATGCGTGCATTTGCTGAGATTAATAGAGCCCTTCAAGAA 180
QY 4036 TCACTAGTTATTAATCTACATGAAACAGTTACTCGTGCCCTTGTATCTCCATGAAAC 4095
Db 181 TCACTAGTTATTAATCTACATGAAACAGTTACTCGTGCCCTTGTATCTCCATGAAAC 240
QY 4096 CAAATCATTCACAGAGATGTAAGAGTCCCAATTTGCTAATTTGACAGACCTGTACAGA 4155
Db 241 CAAATCATTCACAGAGATGTAAGAGTCCCAATTTGCTAATTTGACAGACCTGTACAGA 300
QY 4156 CTAAGAAATTCAGATTTTGGAGCTGCAGCCAGTGGCATCAAAAGAACTGGTCAGGA 4215
Db 301 CTAAGAAATTCAGATTTTGGAGCTGCAGCCAGTGGCATCAAAAGAACTGGTCAGGA 360
QY 4216 GAGTTTCAGGACCAATTTACTGGGGCAATTCGATTTATGGAACCTGAGTACTAAGAGT 4275
Db 361 GAGTTTCAGGACCAATTTACTGGGGCAATTCGATTTATGGAACCTGAGTACTAAGAGT 420
QY 4276 CAACAGTATGGAAGAGAGCTGTGATGTATGAGAGTGTGGCTGTGCTATTTAGAAATGCT 4335
Db 421 CAACAGTATGGAAGAGAGCTGTGATGTATGAGAGTGTGGCTGTGCTATTTAGAAATGCT 480
QY 4336 TGTGCAAAACCAACCATGGAATGAGAAAAACACATCCATCATCTGCTTGTATTTAAG 4395
Db 481 TGTGCAAAACCAACCATGGAATGAGAAAAACACATCCATCATCTGCTTGTATTTAAG 540
QY 4396 ATTGCTAGTGCATCTGCTCCATGATGCCCTTCACATTTGTCTCTGCTTTAGCA--G 4453
Db 541 ATTGCTAGTGCATCTGCTCCATGATGCCCTTCACATTTGTCTCTGCTTTAGCAAGA 600
QY 4454 ATGTGGCTCTCTGCTGTTT--AGAACTCAACCT 4485
Db 601 GTTNGCTCTCTGCTGTTTAAAGAACTCAACCT 633

RESULT 4
B1654958 868 bp mRNA linear EST 12-SEP-2001
LOCUS 603283220F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5327644 5'
DEFINITION mRNA sequence.
ACCESSION B1654958
VERSION B1654958.1 GI:15569194
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 868)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LLM11831 row: 9 column: 05
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High quality sequence stop: 821.

FEATURES  
Location/Qualifiers  
1. 868

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/dev\_stage="5 months"  
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/note="Organ: mammary; Vector: pCMV-Sport6; Site:1; Salt: Site:2; Note: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furch, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."

BASE COUNT 220 a 230 c 264 g 154 t

Query Match 11.1%; Score 583; DB 13; Length 868;  
Best Local Similarity 85.0%; Pred. No. 2.5e-114;  
Matches 664; Conservative 0; Mismatches 115; Indels 2; Gaps 1;

QY 483 CCGCGGTGAGATGAGATTAAGAAACTCTCAAAAGGTTCGACAAAGTGTATG 542  
DB 64 CCGGAATCGAGATGAGATTAAGAAACTCTCAAAAGGTTCGACAAAGTGTATG 123  
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DB 124 CCGGAGAGAGATGATGAGAGAAAGTGAAGGCACTGTATGCGACCTGGAAGCA 183  
QY 603 CGAATGTTGGAAGAAATAGCGAGGCGCTGTGTGTAAACCAATCCAGTTAA 662  
DB 184 CGAGTGTGAGAGAGAGAGAGAGGCGCTGTGTGTAAACCAATCCAGTTAA 243  
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DB 244 AGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 303  
QY 723 TGGCGTTCACCACTCCAAAGCGCGAGCTCTCTCTGGAACCTCCCATCAG 782  
DB 304 TTTCCGTGACCAAGCGCGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363  
QY 783 TGGCAGATGAAATCAGATCTCCAGAGAGTGAAGAGAGAGAGAGAGAGAGAG 842  
DB 364 GCGCTGTGAGAGCGAGATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423  
QY 843 TCAGATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 902  
DB 424 CCGAGATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483  
QY 903 TACCCCTGAG 962  
DB 484 CAGCCAG 543  
QY 963 GCAAGATGAG 1022  
DB 544 GCGAGATGAG 603  
QY 1023 GGTGTTATTTGGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1082  
DB 604 GGTGTTATTTGGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663  
QY 1083 ATTGTGATGCTCCGGGTCTTCACTAGAACCTTCAAGCCCAATGTTAGAGAAAC 1142  
DB 664 GTTGTGATGCTCCGGGTCTTCACTAGAACCTTCAAGCCCAATGTTAGAGAAAC 723  
QY 1143 TTTT-AAAGAAATTTGAGGTGAGAGTTTCTCAGAAATATCAGAGAGAGAGAG 1200  
DB 724 TTTTAAACAATTTGAGGTGAGAGTTTCTCAGAAATATCAGAGAGAGAGAGAGAG 783  
QY 1201 AGATCAAAAGCTCAGTCTGTAACAGCAATCCAGAGAGTTGTTTACGAGATGTA 1260

DB 784 AGATCAAAAGCTCAGTCTGTAACAGCAATCCAGAGAGTTGTTTACGAGATGTA 843  
QY 1261 C 1261  
DB 844 C 844

RESULT 5  
AJ450706 716 bp mRNA linear EST 19-APR-2002  
LOCUS AJ450706 riken1 gallus gallus cdna clone 26c20r1, mRNA sequence.  
DEFINITION AJ450706  
ACCESSION AJ450706  
VERSION AJ450706.1 GI:20217927  
KEYWORDS EST.  
SOURCE chicken.  
ORGANISM Gallus gallus

REFERENCE  
AUTHORS 1 (bases 1 to 716)  
TITLE Buerstedde, J.M.  
JOURNAL Gallus gallus bursal lymphocyte EST  
COMMENT Unpublished (2002)  
Contact: Buerstedde JM, Cellular Immunology  
Heinrich-Pette-Institute  
Martinistr. 52, 20251 Hamburg, Germany  
Email: URL: http://genetics.hpi.uni-hamburg.de/dt4dest.html.

FEATURES  
Location/Qualifiers  
1. 716

source  
/organism="Gallus gallus"  
/db\_xref="taxon:9031"  
/clone="26c20r1"  
/clone\_1lb="riken1"  
/cell\_type="bursal lymphocyte"  
/dev\_stage="2-3 weeks old"  
/note="CB Inbred strain"

BASE COUNT 226 a 132 c 175 g 182 t 1 others

Query Match 10.4%; Score 544; DB 9; Length 716;  
Best Local Similarity 85.8%; Pred. No. 5.7e-106;  
Matches 615; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

QY 3546 GATGAGAGTGAAG 3605  
DB 1 GATGAGAGTGAAG 60  
QY 3606 TGGCTTCCCATATGTTCTCAGCTGAGAGTTGAAAATGAGAGATATCATATTTCA 3665  
DB 61 TGGCTTCCCATATGTTCTCAGCTGAGAGTTGAAAATGAGAGATATCATATTTCA 120  
QY 3666 ACAGATACACCGAG 3725  
DB 121 GCGAGATACCGAG 180  
QY 3726 CACTGATGCTGAAGAGTCAACAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3785  
DB 181 TGCAGATGCTGAAGAGTCAACAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
QY 3786 TCAAGATGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3845  
DB 241 TCAAGATGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3900  
QY 3846 ATCTTTGAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3905  
DB 301 ATCTTTGAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 360  
QY 3906 TCTGATCATCCCAACATCATCATCATCATCATCATCATCATCATCATCATCATCAT 3965  
DB 361 TCTAAACATCTTAAT 420

QY 3966 TCTCTTCATGATGATGGCAGGGGATGCGCTCATTTGCTGAGTAATATGAGC 4025  
 |||||  
 Db 421 CCTCTTCATGATGATGGCAGGGGATGCGCTCATTTGCTGAGTAATATGAGC 480  
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 QY 4026 CTTCAGAAATCAGTATTTACTACTAGCAAGTTCCTCGCTTCTGATCT 4085  
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 Db 481 CTTCAGAAATCAGTATTTACTACTAGCAAGCACTTTACGTGGCTTTCTTACT 540  
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 QY 4086 CCATGAAAACCAATCATTCACAGAGATGTCAAAAGGTGCCAATTTGCTAAATGACAGAC 4145  
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 Db 541 CCATGAGAAATCAGATATTCATAGAGATGTCAAAAGGTGCCAATTTGCTAAATGACAGAC 600  
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 QY 4146 TGTCTGACAGACTAGAAATTTGACATTTTGAGACTGCACGCCAGTGTGCAATCAAAAGAAC 4205  
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 Db 601 AGGTCTAGTATTAAGATTCCTGATTTTGAGCTGCAGCCAGGTGTGCAATCAAAAGAAC 660  
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 QY 4206 TGTGTGAGAGAGATTTGAGGACAAATTCAGCAATTTGATTTGACACCTGA 4262  
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 Db 661 TGTGTGAGAGAGATTTGAGGACAAATTCAGCAATTTGATTTGACACCTGA 716  
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RESULT 6  
 AM499603 530 bp mRNA linear EST 01-MAR-2000  
 LOCUS UI-HF-BP0P-ain-b-12-0-UI.r1 NIH\_MGC\_51 Homo sapiens cDNA clone

DEFINITION IMAGE:3072335 5', mRNA sequence.  
 ACCESSION AM499603  
 VERSION AM499603.1 GI:7111428

KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mhc.nci.nih.gov/  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 530)

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgabs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: M.B. Soares Lab  
 cDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/dbp/image/image.html  
 Seq primer: M13 forward

FEATURES  
 source  
 1..530  
 Location/Qualifiers

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3072335"  
 /clone\_1lb="NIH\_MGC\_51"  
 /tissue\_type="lymph"  
 /cell\_type="germinal center B cells"  
 /lab\_host="DH10B (LT1)"  
 /note="Vector: pT73-Pac; Site.1: NotI; Site.2: Eco RI;  
 Constructed from size fractionated cytoplasmic mRNA  
 (4.4-7.4kb). Directionally cloned. Cells provided by  
 Louis M. Staudt, Ph.D. Library preparation by Maria de  
 Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 141 a 116 c 116 g 157 t  
 ORIGIN  
 Query Match 9.9%; Score 519.8; DB 10; Length 530;  
 Best Local Similarity 99.6%; Pred. No. 8.7e-101;  
 Matches 521; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2268 TCTTGGCGGCTTGTCTTATAGATAGCTGTGTTGGAATTTCCCTGAAATTTATGCC 2327  
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 Db 8 TCTTGGCGGCTTGTCTTATAGATAGCTGTGTTGGAATTTCCCTGAAATTTATGCC 67

QY 2328 TCATATTTGATGATGATGTTTTCACAGCTGACCTGTTGAATCAGGTATAGAAAGCT 2387  
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 Db 68 TCATATTTGATGATGATGATGTTTTCACAGCTGACCTGTTGAATCAGGTATAGAAAGCT 127  
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 QY 2388 GCTGTCCCTCTTAACTCTTCTTGGCAGTCCATGATATATCCACATCAGTGTGGCAA 2447  
 |||||  
 Db 128 GCTGTCCCTCTTAACTCTTCTTGGCAGTCCATGATATATATCCACATCAGTGTGGCAA 187  
 |||||  
 QY 2448 ACTTCCAGAGAGATCTACTTGAATTCGCAAGATGTTACTACTACCCATGCTT 2507  
 |||||  
 Db 188 ACTTCCAGAGAGATCTACTTGAATTCGCAAGATGTTACTACTACCCATGCTT 247  
 |||||  
 QY 2508 TTCAAACTGTTTAAAGTGTGAGTGTTCCTGATTCACATCTTCCACAGATGCTGC 2567  
 |||||  
 Db 248 TTCAAACTGTTTAAAGTGTGAGTGTTCCTGATTCACATCTTCCACAGATGCTGC 307  
 |||||  
 QY 2568 CCGTTGATGCTTATTCACATGAGTGGAAATTCGCCGAAGCCATCCAGTTGGCGGTAGA 2627  
 |||||  
 Db 308 CCGTTGATGCTTATTCACATGAGTGGAAATTCGCCGAAGCCATCCAGTTGGCGGTAGA 367  
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 QY 2628 AGACACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2687  
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 Db 368 AGACACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 427  
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 QY 2688 GGAACCCAG 2747  
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 Db 428 GGAACCCAG 487  
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RESULT 7  
 B1656574 719 bp mRNA linear EST 12-SEP-2001  
 LOCUS B1656574  
 DEFINITION mRNA sequence.  
 ACCESSION B1656574  
 VERSION B1656574.1 GI:15570810

KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE NIH-MGC http://mhc.nci.nih.gov/  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 719)

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgabs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth  
 Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: L14M1835 row: 0 column: 06  
 High quality sequence stop: 719.  
 Location/Qualifiers

FEATURES  
 source  
 1..719  
 Location/Qualifiers

/organism="Mus musculus"  
 /strain="NMRI"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5329373"  
 /clone\_1lb="NCI\_CGAP Mam4"  
 /tissue\_type="tumor, gross tissue"  
 /dev stage="5 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: SalI;



Db	486	TGTTTCAACTAGAACCTTCACAGCCCAATGTATTGGAGAAAAAAGCTTTAAAGAATTTTGAGC	545
Oy	1160	TTGAGAGTTTGTTCAGAAATATCACAGTAGCGTAGTCAAAGATCAAAGTCATCATTCG	1219
Db	546	TTGGAGAG-TTGGTCTCAGAAAATAT-ACAAGTAGCCGTA-CTCAGGGTTCAAAGTGCATCTC	601
Oy	1220	GTAACACCATC	1230
Db	602	GTAACACCATC	612
RESULT 9			
LOCUS	BE981914		
DEFINITION	714 bp mRNA linear EST 29-APR-2002		
ACCESSION	U1-M-CG0P-bde-g-02-0-U1.s1 NIH-BMAP_Ret4_S2 Mus musculus cDNA clone		
VERSION	BE981914		
KEYWORDS	BE981914.1 GI:10651525		
SOURCE	EST.		
ORGANISM	house mouse,		
	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 714)		
	Bonaldo,M.F., Lennon,G. and Soares,M.B.		
JOURNAL	Normalization and subtraction: two approaches to facilitate gene		
MEDLINE	discovery		
COMMENT	Genome Res. 6 (9), 791-806 (1996)		
	97/044477		
	Contact: Chin, H		
	National Institute of Mental Health		
	6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD		
	20892-9643, USA		
	Tel.: 301 443 1706		
	Fax: 301 443 9890		
	Email: mestr@mail.nih.gov		
	Oligo-dt track not found, Not I site shown in beginning of sequence		
	is likely internal to the message. cDNA Library Preparation: M.B.		
	Soares lab clone distribution: Researchers may obtain BMAP cDNA		
	clones from RESEARCH GENERICS. It should be noted that Bento Soares		
	is generating a small number of additional specialized		
	non-redundant arrays of BMAP cDNAs whose availability will be		
	considered under appropriate and limited collaborative arrangements		
	The tissue for this library was contributed by Dr. Xin-Yuan Fu,		
	Yale University School of Medicine The following repetitive		
	elements were found in this cDNA sequence: 1-49,		
	>GC-rich#low-complexity		
	Seq primer: M13 Forward		
	POLYA-No.		

FEATURES	source	Location/Qualifiers
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		/strain="C57Bl/6J"
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		/clone="U1-M-CG0P-bde-g-02-0-U1"
		/clone_1lb="NIH-BMAP_Ret4_S2"
		/lab_host="DH10B (Life Technologies)"
		/note="Vector: pRT73D-Pac (Pharmacia) with a modified polylinker. Site.1: Not I; Site.2: Eco RI; The NIH-BMAP_Ret4_S2 library is a subcloned library ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainrest.eng.uiowa.edu. The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine"
		TAG_SEQ=None found"
BASE COUNT	169 a	225 g 116 t
ORIGIN	203 c	1 others
Query Match	9.48%	Score 494.2; DB 12; Length 714;
Best Local Similarity	84.1%;	Pred. No. 2.7e-95;

Matches	581;	Conservative	0;	Mismatches	108;	Indels	2;	Gaps	2;
QY	427	CCCCAGCCCGGGAGAGAGCGGGCGCCCGCCCGCCGACGCTGTCTCTCGACGCGCGCCCGCC							486
Db	8	CGCGGACACGGCGCCCGGAGCCCGCGCGGGGGCCCGAGCCGCTCTGCGAGCGCGCCCTTC							67
QY	487	GGTGTGATGATGGAGAAATTAAGAAACCTCTCAAAGGGTTGGCAAGATGGATGATGCTTCA							546
Db	68	GGTCGAGGATGGAGAAATTAAGAAACCTCTCAAAGGACTGCAACAGATGAGAGATGCGCCG							127
QY	547	GAGGACGAAATGATCAGGAGAAACTGAAGGCAACCTTATGCCAGCTCGGAGAGCAGAA							606
Db	128	GAGGAGAAATGATTCGGGAGAACGCTCAAGCGACCTTATGCCGCTCGAAGACAG							187
QY	607	TGCTTGGAAAGAGAAATAGCGAGGGCCCTGTGTGTGTTAAACCAATCCAGTTAAAGGA							666
Db	188	TGCTTGGAGAGAGAAACAGGAGAGGCCCTGTGTGTGTTGAAGCCAACTCTTATTAAGGA							247
QY	667	GATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCCAGAGAGAGTCCAGGCAAGTGC							726
Db	248	GATGGATCTGAAATGAATCACTTAGGCACTAGGCCCAAGAGAGAGGTCACGAGGTTCC							307
QY	727	GCTTCACCACTTCCAAAGGCGGACGAGCTCCTTCTCTGGCAACTCCCATCAGAGGTGC							786
Db	308	GCTGCACCAAGCCCCCAAGGGCCGACGAGAGCCCATCTCTTGCGAGCTCTCCGTCAGGGCC							367
QY	787	ACAATGAATCAGATCTCCAGAGTAAAGGAAAGATTTCCCGAGTGCCTTTTCAG							846
Db	368	TCGGTGAAGCCGGATATCCCGACGAGGTGAGAGGAAAGAGTGTCCCGGTGCTTTCAG							427
QY	847	AGTGGCAGATCACACCAACCCC -GAAGAGCCCCCTTACACAGATGGCTTCTACCATATAG							905
Db	428	AGTGGCAGAAATCACACCAACCCCNAGAGAGCCCGGACACGGATGGCTTCTCCCGCTACAG							487
QY	906	CCCTGAGGAAACAAACCCGCGGTGTTAAACAAAGTGTGGGGCGACAGATGCTTAGTCA							965
Db	488	CCCGAGAGAGACGAGAGCCCGCCCGGTGAACAAAGTGTGAGAGCGACAGGCTGTACTCTGCA							547
QY	966	GCAGATAGGGCTTAACCTTTCTCTGATTTGAGAGACAGCCCGACAGCAATTAATACCGGGT							1025
Db	548	GCAGATAGGACCAACCTTTCTCTGATTTGAGAGACAGTCCAGACAAATTAATACCGGGT							607
QY	1026	GTTTATTTGGGCTCAGAACTGCAAGTGTGACAGTGGAAACATTTCTGTATTCATCTGCTATT							1085
Db	608	GTTTATTTGGGCTCAGAACTGCAAGTGTGGGCGTGGACATTTCTGTA -TCACTCTTCTGT							666
QY	1086	TGTGATGCTCCGGGTTTCAACTAGAACCT 1116							
Db	667	TGTGATGCTCCGGGTTTCAAGTAAACCT 697							

RESULT	10
LOCUS	AW916314
DEFINITION	AW916314 624 bp mRNA linear EST 25-MAY-2000
ACCESSION	EST347618 Rat gene index, normalized rat, norvegicus, Bento Soares
VERSION	Rattus norvegicus cDNA Clone RGIDN30 5' end, mRNA sequence.
KEYWORDS	AW916314 AW916314..1 GI:8082037
SOURCE	EST.
ORGANISM	Norway rat. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 624)
AUTHORS	Lee,N.H., Glodok,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
TITLE	Rat Genome Project: Generation of a Rat EST (RESTR) Catalog & Rat Gene Index
JOURNAL	Unpublished (1998)
COMMENT	Contact: Lee, NH The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA

Tel: (301)-838-3529  
Fax: (301)-838-0208  
Email: [mhleee@tyr.org](mailto:mhleee@tyr.org)  
This clone is available through the ATCC, contact the ATCC  
tel#703-365-2700 for further information  
Seq primer: M13 Reverse.

## FEATURES

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1. .624
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RGIND30"
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Bento Soares"
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/lab_host="SOLR"
/notes="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Estimated insert size approx.1 kb"
148 a 162 c 157 g 157 t

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DEFINITION	UI-M-CG0b-bdc-f-06-0-UI.s1 NRH_BAP_Ret4_s2 Mus musculus cDNA clone
ACCESSION	UI-M-CG0b-bdc-f-06-0-UI 3', mRNA sequence.
VERSION	BE981478
KEYWORDS	BE981478.1 GI:10650625
SOURCE	EST.
ORGANISM	house mouse. Mus musculus.

## FEATURES

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source
1. .714
/organism="Mus musculus"
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/clone_1id="NIH_BMAP_Ret4_S2"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pUT73d-Pac (Pharmacia)"
polylinker: site_1: Not I; site_2: Eco RI; The
NIH_BMAP_Ret4-S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainrest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
TAG_SEQ=None found"
168 a 203 c 226 g 116 t 1 others

```











GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2002, 16:20:45 ; Search time 60 Seconds  
(without alignments)  
5192.387 Million cell updates/sec

Title: US-09-697-898-2

Perfect score: 7825  
Sequence: 1 MAAAGNRASSSGFPGARAT.....PODRPSELKHPVFRRTW 1512

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTRMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_undefined:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	595.5	7.6	690	10 Q40541	Q40541 nicotiana t
2	595.5	7.6	1230	3 Q9HFT9	Q9HFT9 cryptococcu
3	591.5	7.6	651	10 Q9EP36	Q9EP36 arabidopsis
4	587.5	7.5	642	10 Q22041	Q22041 arabidopsis
5	578	7.4	651	10 Q22042	Q22042 arabidopsis
6	576.5	7.4	585	10 Q9C7M0	Q9C7M0 arabidopsis
7	576	7.4	376	10 Q22040	Q22040 arabidopsis
8	576	7.4	661	10 Q22039	Q22039 arabidopsis
9	562.5	7.2	942	5 Q96611	Q96611 dictyosteli
10	558.5	7.1	591	10 Q82667	Q82667 brassica na
11	557.5	7.1	594	4 Q96H89	Q96H89 homo sapien
12	552.5	7.1	1338	3 Q60030	Q60030 kluyveromyc
13	542	6.9	666	3 Q42625	Q42625 neurospora
14	539.5	6.9	619	4 Q9NKC3	Q9NKC3 homo sapien
15	538.5	6.9	883	10 Q9CAD5	Q9CAD5 arabidopsis
16	536.5	6.9	609	10 Q8W582	Q8W582 arabidopsis

17	531.5	6.8	608	10 Q9LPH2	Q9LPH2 arabidopsis
18	531	6.8	608	10 Q9ZRF7	Q9ZRF7 arabidopsis
19	531	6.8	653	10 Q9LIM7	Q9LIM7 oryza sativ
20	531	6.8	1166	3 Q9P4E0	Q9P4E0 ustilago ma
21	523	6.7	823	3 Q9HFR3	Q9HFR3 pneumocysti
22	521.5	6.7	1832	3 Q8TGH8	Q8TGH8 podospora a
23	484	6.2	652	10 Q04030	Q04030 arabidopsis
24	483	6.2	582	10 Q82649	Q82649 arabidopsis
25	480	6.1	716	10 Q9C5H5	Q9C5H5 arabidopsis
26	479	6.1	716	10 Q932H4	Q932H4 arabidopsis
27	477	6.1	1612	5 Q9VE37	Q9VE37 drosophila
28	473	6.0	1497	5 Q95YH6	Q95YH6 drosophila
29	473	6.0	1571	5 Q95YH7	Q95YH7 drosophila
30	472	6.0	847	10 Q8W5G2	Q8W5G2 oryza sativ
31	467.5	6.0	608	10 Q8W4N5	Q8W4N5 arabidopsis
32	461.5	5.9	608	10 Q39020	Q39020 arabidopsis
33	461.5	5.9	608	10 Q81470	Q81470 arabidopsis
34	455.5	5.8	650	5 Q24458	Q24458 drosophila
35	455.5	5.8	1310	5 Q9VDS9	Q9VDS9 drosophila
36	449.5	5.7	376	10 Q9FKZ5	Q9FKZ5 arabidopsis
37	449.5	5.7	535	10 Q82650	Q82650 arabidopsis
38	447	5.7	773	10 Q81472	Q81472 arabidopsis
39	446	5.7	372	10 Q23721	Q23721 arabidopsis
40	445.5	5.7	560	10 Q9WOT3	Q9WOT3 arabidopsis
41	443.5	5.7	1289	11 Q9WTR2	Q9WTR2 mus musculu
42	442.5	5.7	1368	10 Q81809	Q81809 arabidopsis
43	441.5	5.6	1368	10 Q9LJD8	Q9LJD8 arabidopsis
44	439	5.6	575	10 Q82668	Q82668 brassica na
45	437.5	5.6	1299	10 Q9STED0	Q9STED0 brassica na

## ALIGNMENTS

### RESULT 1

Q40541 ID Q40541 PRELIMINARY; PRT; 690 AA.  
AC Q40541;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
DE Protein kinase.  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Machida Y.;  
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9330268; PubMed=8336712;  
RA Banno H., Hirano K., Nakamura T., Irie K., Nomoto S., Matsumoto K.,  
RA Machida Y.;  
RT "NPK1, a tobacco gene that encodes a protein with a domain homologous  
to yeast BCK1, STE11, and Byr2 protein kinases.";  
RL Mol. Cell. Biol. 13:4745-4752(1993).  
CC -!- SIMILARITY: BELONGS TO THE SHR/THR FAMILY OF PROTEIN KINASES.  
DR EMBL; D26601; BA05648.1; -;  
DR HSSP; P24941; IAO1.  
DR InterPro; IPR000719; Euk\_pkinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Euk\_pkinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 690 AA; 76241 MW; 2F9C2A3AA31C6094 CRC64;

[illegible]

RESULT 2	09HFT9	ID	09HFT9	PRELIMINARY;	PRT; 1230 AA.
	AC	09HFT9;			
	DT	01-MAR-2001 (Tremblrel. 16, Created)			
	DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)			
	DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)			
	DE	Stellalpha protein.			
	GN	STELLAPHA.			
	OS	Cryptococcus neoformans (Filobasidiella neoformans).			
	OC	Eukaryota; Fungi; Basidiomycota; Hymenomyces; Heterobasidiomycetes;			
	OC	Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.			
	OX	NCBI_TaxID=5207;			
	RN	[1]			
	RP	SEQUENCE FROM N.A.			
	RA	MEDLINE=21195876; PubMed=11298287;			
	RA	Clarke D.L., Woodlee G.L., McClelland C.M., Seymour T.S., Wickes B.L.;			
	RT	"The Cryptococcus neoformans STELLalpha gene is similar to other			
	RT	fungal mitogen activated protein kinase kinase (MAPKK) genes			
	RT	but is mating type specific."			
	RL	MOL. Microbiol. 40:200-213(2001).			
	DR	EMBL; AF294841; AAC30205.1; "-.			
	DR	HSSP: Q63450; 1A06.			
	DR	InterPro: IPR000719; Euk_Pkinase.			
	DR	InterPro: IPR001660; SAM.			
	DR	InterPro: IPR002290; Ser_thr_Pkinase.			
	DR	InterPro: IPR001245; Tyr_Pkinase.			
	DR	Pfam: PF00069; Pkinase; 1.			
	DR	Pfam: PF00536; SAM; 1.			
	DR	PRINTS: PR00109; TYRKINASE.			
	DR	ProDom: PD000001; Euk_Pkinase; 1.			
	DR	SMART: SM00454; SAM; 1.			
	DR	SMART: SM00220; S_TKC; 1.			
	DR	SMART: SM00219; TYRKC; 1.			
	DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.			
	DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.			
	DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.			
	KW	ATP-binding; Transferase.			
	SO	SEQUENCE 1230 AA; 134937 MW; 99955068AD6A40C4 CRC64;			
	Query Match	7.6%; Score 595.5; DB 3; Length 1230;			
	Best Local Similarity	23.1%; Pred. No. 4.2e-28;			
	Matches 298; Conservative 188; Mismatches 455;				
	Indels 349; Gaps 57;				
OY	466	KLHH-HCM5IAEGRNRREPLICLGRSKNRSHFYSHELSSPYDSSLSRAAQOQTVQ	524		
Db	9	RLHHTHSSV-----SPRASNDVAP--SSPPNPQHOLAASPLVA	47		

QY	523	QOPLAGSRNOSNF--NLTHGTQOIPRAYD-LAEPHIOVPGHELVCLSESRMNNRE	581
Db	48	NSPNCASKITTKGSSLSSTAHGGLVYRPESTPLRLSPGEEFSAVL-----GNGSGOE	101
QY	582	MLARLRSH-----DVSAGLLANGESTGNSGSGSPSGCATSGSSQTSIG	629
Db	102	LTFPLNHCQGYLAIFOKNDINGKILL-DLDMT-----AKSMGIGKISERYRLG	152
QY	630	DVEVACCSVLSNWCADPVYKYVAALKTL-----RAMLYTTPCHSLAERI-KLORLL	680
Db	153	GJKDLRRCVADESIKAPFQSRYSERBTLPLSPHSNVLRLKMPCCSSASRLKQRYL	212
QY	681	QP-----VDTLIVKCADANSTQSLSL-----	703
Db	213	REPPDLOGHMPRLLSHSLGIAITDIT-----HIIHTNSKIEVYIQONPGOPQSMPT	267
QY	704	--STLELCKQAGELAVR-----ELKAGSIGIGVYUYNLCIJGNDTESNNQE	753
Db	268	KRSDSLTLC--AAPSRNNGRSPSRHFGGCKSQTDGL-----TTLNLTIDROYPSSTMMN	321
QY	754	L-LGRCLCLDR-----LLEFP--AEFYPHIVSD-----VSO	783
Db	322	VTLREDCHLQREBRLPLSHQVPHSRNAFASPKHTLSGRCPLARGDTTSHQSGPALAQ	381
QY	784	AEFVEIRYKLLS-----LTFALQSL-----DNSHKNV-----GKL	815
Db	382	DSPPVYRISNTYNTNKEISQDGLKOPFYVKSLSIOSHLIAGVSDMSHDVTDGFRKPKKA	441
QY	816	SRRIYLSARWTVY--PHVFS-----KLLEMLSVSSSTPFTNRRLRLMAIADEVEIA	866
Db	442	SVPLIVWSSSDISAVNANPALSLADLRQLKFIETEDTIRT--VAVMHVTSGEVLL	498
QY	867	E-----AIOUGVEDTLD--GOO--DSFLQASVPNNYLETT--ENSSP-----ECT	905
Db	499	EBALAKFKFGGIGHSPPDYGEDDGDGLTIGHEVYTESIPDDSSKRLSEFNLLKTT	558
QY	906	VHLEKTG--KGLCATKUS--ASSEDISERLASISVGPSSTTTTTTTOEKPKNYQKG	960
Db	559	FREESTAIODKGLFLRKORKMOKRNKIOFGE--TPPSPSPSTPLTLGPHLSIOCKS	617
QY	961	RPHSOCINS-----PLSHSQ-----LMPALSTPSSSTPSPAGTATDVSKHRLQGF	1009
Db	618	QPTSGANSSSRLSTLTHKGNRRASMTSVMSGLGVPITLTPSPGNGL-----RLTGS	672
QY	1010	IPCRIIPSAPOQRFSLQFHNCCEBKDKSLSPVTFQSRPLPSNIRPKPS-----	1063
Db	673	V-----HSHKSMXNFPFGHRP-PSELISNLTLOYFPAK--KSDVKAKHSLRLSG	722
QY	1064	-----RPTPGNTSKQD-----PSKNSMT-----	1082
Db	723	GTVAAVKKSGIYEGDSTPDHMSKPCDNOPSLPLPFPEESQDTLDSLOAFASSTPVHLSPK	782
QY	1083	-----LDLNSSSKCQDSF-----GSSSNMNAVIPSDETVTPVPEKCRLOY----	1124
Db	783	HTVALRRRRDSSSSSHSTSMLOTRRNDSHDTLSLTVDE--ITAEYENRRVSTIORG	840
QY	1125	---NTELNSJIEDLEASMPSSDTTVTFKSEVAULSPKAEKENDDTYKDVVHNKCKEK	1180
Db	841	DYIEETEDSSSTIEG---DTLPQDDSKGYLRAICSDSNKLVSCKSGSYQDSIDQ--QHE	895
QY	1181	MEAEDEEALAIAMMASASODALPIVPOLOVENGEDIIIIQODTPETLPGHTAKOPYRED	1240
Db	896	LEDEEDKTL-----DDD-----EEEE--EEEEENEOGKAPTSGSKRI	933
QY	1241	TEWLKGOOIGIGAFSSCQAOOVGCTLMAVQVYVYRNTSSEOE---EYVALABEIRMA	1297
Db	934	IKWIGALIGASFSSVYLVGMDAGSGLLMAVQVELSMGASANERKRSMLSALREIEL	993
QY	1298	MSHLNHPNIIIRMLGATCEKSNYNLPLEMMAGSGVAHLISKYAFKESVYINTEDBLGL	1357
Db	994	LKELOHENIVQVLDSVDANHLNITLLEYVPGGSVAALLNNYCAFEBALYRNFVROLTGL	1053
QY	1358	SYLHENOIIHRDVKANLIDSTGORLRLADGGAARLA--SKGTGAGEFOGLGTIAFM	1416

QY	816	SRRIYLSARWVTVV----	PHVES-----	KLEMLSVSSSTFTFRRRRLMA	IADEVIEA	866
Db	382	DSPVNRISNTVNTKELISQ	DLKOPFVMSKLS	SOSHLAGVSDMSHDVYTG	FFRPGKIA	441
QY	442	SVPLVYMWSSSDISAVAN	PALSLADLRQVLF	INTEDDTRT---	VAVMHTVSGVELL	498
QY	867	E-----	AIOLGVEDTLD--GOO--	DSTLQASVPNNITLTT--	ENSSP-----	ECT 905
Db	499	ERALKKFGKFGTGISPD	YVEDEGDGTL	ELGWEVYESTPDESSKPL	SEFNLIKTCY	558
QY	906	VHEKTEG---	KGLCATKLS--	ASSEDISERLASISVGPSST	TTTTTTTTTTTDEGR	PMVOTGK 960
Db	559	FIREGTAIDOKKLF	LKKOKRMRKKNID	FFEE--TPPMSST	SPLITGRPLSLVQGS	617
QY	961	RPHSOLNS----	SPLSHSQ-----	LMFALSTPSSSTFSPV	AGATVDSKHNLOGF	1009
Db	618	QPTSGSAFSSSRSLST	LTHKGNRRASMISV	MGGLGVPINTL	PLSPQGNL-----	RLTGS 672
QY	1010	IPCRIPLASPOQRKFS	LQFHNCEBNKDSKLS	PFYQSRPLPSSN	HNRPDS-----	1063
Db	673	V-----	HSHEKKSMYNFEGHRP-	PSELISNHLTDY	FPSPAK--KSDVEKARH	SLRLSG 722
QY	1064	-----	RPPTGNTSKROG--	-----	PSKRSMT-----	1082
Db	723	GTVAAKKGSTYEGDST	PDHMSKRCQDNOP	SLPFPERSQDTLS	DISLQAFASSTPYHLS	SRPK 782
QY	1083	-----	LDLNSSSKDDSF-----	GCSNSSNAVIPS	DETVEETVPEEKCR	LDV--- 1124
QY	1125	-----	NPELNSSTIEDLEAS	MPSSDTPYFPEKS	SVAYLSPKAKANDDQY	KQDVHNNQCKRKK 1180
Db	783	HTVALRRRRDSDSSSR	SHTSMLOTRRNHD	HDTSLLTVDE--	ITAEVENRRVSTIOGR	840
QY	841	DYIETEDSSSTIEG--	DTLPDDDSKGV	LRAICSDSNKLVS	GSKSYQDSDSDIO--	QHE 895
QY	1181	MEAESEELALIMASAS	ODALPPIPOLV	ENGEDI	IIIIQDTPETLPHTRAKO	PYRED 1240
Db	896	LEDEDEDKL-----	DDD-----	EEEE--	EEBEDNDEGAKTYS	GSKI 933
QY	1241	TEWLKGOOIGLCA	SSCQAOADVGTCTL	MAVQVTVYRNT	SSOE---EVEALABE	TRM 1297
Db	934	IKWIGALIGAGS	FSFSYVLGMDA	OGGLMAVQVEL	SLGSSANENRKRK	SMLSALREIEL 993
QY	1298	MSHLNHPNITIRL	GAICEKSNYLN	PLEMMAGSV	YHLLSKYAFKESVY	INTBOLLGL 1357
Db	994	LKELOHENIVQ	LDSSVDANHN	ITLEIYVPGGS	VAAALLNNYGA	FEDALVRNFVOITGL 1053
QY	1358	SYLHENOIHRD	YVKANLIDSTG	ORLRIADGA	ARULA--SKGTGAGE	FOGOLLTIAFM 1416

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Db 1054 NYLHMGIVHNRDIGNANILVDNKG-GIKISDFGISKVENSLLTGTNTNPSLOGSVFW 1112
QY 1417 APEVLGQOYGRSCDYSVGCATIEEMACAPPNNAEKSHNLIFKIASATTAPISPH 1476
Db 1113 APEVYQOTSVSPRADIMSVGCLVEMITGTHPM---ADLTQMAIFRIGS-LARPAPSD 1168
QY 1477 LSPGLRDVALRCLELOPQDRPPSRELLKHP 1506
Db 1169 ISVOADEFLKRTFEIEHAKRPQAQLKHP 1198

RESULT 3
Q9F236 PRELIMINARY; PRT; 651 AA.
AC Q9F236;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE NP1-related protein kinase 2.
GN T24C10.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altieri H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA Buehler E., Chao Q., Chin C., Chlou J., Choi E., Gonzalez A.,
RA Hough B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
RA Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.,
RA Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC064840; AAC00876.1;
DR HSSP: P24941; 1A01.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Transferase.
SQ SEQUENCE 651 AA; 71848 MW; 0204655E1F9E918E CRC64;

Query Match 7.6%; Score 591.5; DB 10; Length 651;
Best Local Similarity 43.3%; Pred. No. 2.9e-28;
Matches 119; Conservative 55; Mismatches 90; Indels 11; Gaps 5;

QY 1234 KQPYREDTEMLKGOIGLGFSSCYQADVGTGLMAVKQVTVYRNTSSQ--EEVEAL 1291
Db 63 KPIR-----WRKGQLIGRGAFTYMGMDSCGELLAVKQVLTLSNCAKSEKTAHQIQL 118
QY 1292 REIRBMASHLNHPNITRMIGATCEKSNYLFIFEMAGGSVAHLISKGAKRESVINYTE 1351
Db 119 EEEVKLLKLNISHPNIVYLTGTVREDETLLILEFVPGSGISSLLEKFGAPESVVRYYTN 178
QY 1352 QLLRGSLYLHENQIIHRDVGANLLIDSTGQRLRIADFGAARLASGTGAGEFQGLG 1411
Db 179 QLLGLELYLNHAIHMDIGANILVDNKG-CIKLADFGASKOVAELATISG--AKSMKG 235
QY 1412 TIAFMAPEVLRGQOYGRSCDYSVGCATIEEMACAPPNNAEKSHNLIFKIASATTAP 1471
Db 236 TTYWMAPEVILQTHGSHFSADIMSVGCTVIEWYTGKAPWS--QYKETAIAIFHIGTKSHP 293
QY 1472 SIPSHLSPGLRDVALRCLELOPQDRPPSRELLKHP 1506
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Db 294 PIPDNISSDANDELLKCLQOEPNLRPTASELLKHP 328

RESULT 4
Q22041 PRELIMINARY; PRT; 642 AA.
AC Q22041;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NP1-related protein kinase 2 (Fragment).
GN AMP2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-COL-0;
RA MEDLINE-97408932; PubMed=9263451;
RA Nishihama R., Hano H., Kawahara E., Irie K., Machida Y.;
RT "Possible involvement of differential splicing in regulation of the
RT activity of Arabidopsis ANP1 that is related to mitogen-activated
RT protein kinase kinase kinases (MAPKKKs).";
RL Plant J. 12:39-48(1997).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB000798; BAA21856.1;
DR HSSP: P24941; 1A01.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Kinase; Serine/threonine-protein kinase.
FW NON_TER 1
SQ SEQUENCE 642 AA; 70786 MW; C277182DD79002E3 CRC64;

Query Match 7.5%; Score 587.5; DB 10; Length 642;
Best Local Similarity 42.9%; Pred. No. 4.9e-28;
Matches 118; Conservative 55; Mismatches 91; Indels 11; Gaps 5;

QY 1234 KQPYREDTEMLKGOIGLGFSSCYQADVGTGLMAVKQVTVYRNTSSQ--EEVEAL 1291
Db 54 KPIR-----WRKGQLIGRGAFTYMGMDSCGELLAVKQVLTLSNCAKSEKTAHQIQL 109
QY 1292 REIRBMASHLNHPNITRMIGATCEKSNYLFIFEMAGGSVAHLISKGAKRESVINYTE 1351
Db 110 EEEVKLLKLNISHPNIVYLTGTVREDETLLILEFVPGSGISSLLEKFGAPESVVRYYTN 169
QY 1352 QLLRGSLYLHENQIIHRDVGANLLIDSTGQRLRIADFGAARLASGTGAGEFQGLG 1411
Db 170 QLLGLELYLNHAIHMDIGANILVDNKG-CIKLADFGASKOVAELATISG--AKSMKG 226
QY 1412 TIAFMAPEVLRGQOYGRSCDYSVGCATIEEMACAPPNNAEKSHNLIFKIASATTAP 1471
Db 227 TTYWMAPEVILQTHGSHFSADIMSVGCTVIEWYTGKAPWS--QYKETAIAIFHIGTKSHP 284
QY 1472 SIPSHLSPGLRDVALRCLELOPQDRPPSRELLKHP 1506
Db 285 PIPDNISSDANDELLKCLQOEPNLRPTASELLKHP 319

RESULT 5
Q22042 PRELIMINARY; PRT; 651 AA.
AC Q22042;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
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DT	01-JAN-1998 (TREMBlrel. 05, last sequence update)
DE	01-MAR-2002 (TREMBlrel. 20, last annotation update)
DT	NPKI-related protein kinase 3 (A79306030/E24F17_1).
GN	ANP3 OR F24F17.1.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
CC	Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
CC	eucosids II: Brassicales: Brassicaceae: Arabidopsis.
OX	NCBI_taxid=3702;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=COL-0;
RX	MEDLINE=97408932; PubMed=9263451;
RA	Nishihama R., Banno H., Kawahara E., Irie K., Machida Y.;
RT	"Possible involvement of differential splicing in regulation of the
RT	activity of Arabidopsis ANP1 that is related to mitogen-activated
RT	protein kinase kinase kinases (MAPKKs).";
RL	Plant J. 12:39-48(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV. COLUMBIA;
RA	Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA	Maiti R., Roming C.M., Koo H., Fujii C.Y., Uteback T.R.,
RA	Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT	"Arabidopsis thaliana chromosome III BAC F24F17 genomic sequence.";
RT	Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RA	Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
RA	Carinanci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA	Isida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA	Lee J.M., Lin J., Miranda M., Narisaka M., Nguyen M., Onodera C.S.,
RA	Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA	Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA	Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT	"Arabidopsis cDNA clones.";
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC	EMBL; AB000799; BAA11857.1; -
DR	EMBL; AC068073; AAF66131.1; -
DR	EMBL; AY069917; AAL47465.1; -
DR	HSSP; P24941; 1A01.
DR	InterPro: IPR000719; Euk_pkinase.
DR	InterPro: IPR002290; Ser_thr_pkinase.
DR	Pfam: PF00069; pkinase: 1
DR	ProDom: PPD00001; Euk_pkinase: 1.
DR	SMART; SM00220; S_Trc; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SO	SEQUENCE 651 AA; 71654 MW; E8BDF683CE31268 CRC64;
Query Match	7.4%; Score 578; DB 10; Length 651;
Best Local Similarity	40.7%; Pred. No. 2e-27;
Matches 116; Conservative 57; Mismatches 102; Indels 10; Gaps	
QY	1224 PETLDGHTKAKOPRYEDDEWMLKGOOLIGLAFSSCCQAQADVCGTILMAVQVYVRRNTSS 1283
DB	52 PGLGLAPRKEEP--SIRMRGELIGCGAFGRVYMGMLDGGELLAIQVILAPISASAK 108
OY	1284 QEEV--VEALREIRIMMSHLINPITIRMGIGACCKSNYLLFTEMAGGSVANHLSKYGAF 1341
DB	109 EKTGSHIRELEBEVOLLKNSHPNIVRYILGYTRRESDSLNIIMEFPVGGISLSLEKFGSF 168
OY	1342 KESVINTTEQLRLGSLYENQIIRHDYKGANLLIDSTGQRLRIADFGAARLASKGTG 1401
DB	169 PEPVIMTKQKOLLGLELYHNNGIMHRIKGANIIVDNKG-CIRLADFASKKVELATV 227
OY	1402 AGEFQGLGTLIAFAPRYLRQQYGRGSDVSVGCATIEAMCARNPMAEKRSHNLALI 1461
DB	228 NG--AKSKNGPRPYMAPEVILLOTGHSFSDIVSVCTVEMATGPRPMG--BOYQOFAV 283

**RESULT 6**

99C7M0 PRELIMINARY; PRT; 585 AA.

ID 09C7M0  
AC 09C7M0;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE NPkI-related protein kinase, putative.  
F14C21.49.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
NCBI\_TaxID=3702;  
[1]  
RN RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RX MEDLINE=21016719; PubMed=11130712;

RA Theologis A., Eckert J.R., Palm C.J., Federspiel N.A., Kaul S.,  
RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,  
RA Buehlner E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
RA Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
RA Gali J.E., Goldsmith A.D., Haas B., Hansen N., Khan S., Khaykin E.,  
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Knap S., Khaykin E.,  
RA Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A., Lam B.,  
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Matli R., Marziali A.,  
RA Miltscher J., Miranda M., Nguyen M., Niernm W.C., Osborne B.I.,  
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
RA Sakano H., Salazar S.L., Schwartz G., Toriumi M.J., Town C.D.,  
RA Sun H., Tallon L.J., Tambunga G., Tortum M.J., Town C.D.,  
RA Uterback T., Van Aken S., Vaysberg M., Vysockaja V.S., Walker M.,  
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
RT thaliana".

RL Nature 408:816-820(2000).  
DR EMBL; AC069144; AAC51109.1; -.  
DR HSSP; P24941; IAQ1.  
DR InterPro; IPRO00719; Euk\_pkinase.  
DR InterPro; IPRO02290; Ser\_thr.pkinase.  
DR InterPro; IPRO01245; Tyr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PRK0109; TYRKINSE.  
DR ProDom; PD000001; Euk\_pkinase; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR SMART; SM00219; Tyrcg; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; transferase.  
SQ SEQUENCE 585 AA; 64716 MW; EFACGCF2452A0166 CRC64;

Query Match 7.4%; Score 576.5; DB 10; Length 585;  
Best local Similarity 42.9%; Pred. No. 2.1e-27;  
Matches 117; Conservative 55; Mismatches 90; Indels 11; Gaps 5

OY 1234 KQRYEDFEWMLGGQOIGCAFSSCGAOADVGCTLMAYKVQVYNNRNTSEO--EEVEAL 1291  
DB 63 KPPIR-----WRKGOLIGRAFAGFTVMGMNDSGELLAKVYLITSNCAKEKETQAHOIEL 118  
OY 1292 REEIRRMASHLNPTIIRMJLGATCEKSNTNLFEEMNAGGSVAHLISKYGAFKESVIYNTE 1351  
DB 119 EEVEALKMLKLSHPNVIVRYGLTVREDETLLILLEFPFGSGISSLLLEKFAGFAPESSVRYTYN 178  
OY 1352 QLRLSLVTHENQITHRDYKANLLIDSTGQRRLRADFGAAARLASKGTGAGEFOGQLIG 1411  
DB 179 OLLEILEYHNHAIARDIKGANIIIVDDNG--CIKLADFAGSKQVELAITISG--AKSMKG 235

QY	1412	TAFMAPEVLNRGOQVGRSGDWSVCCATITEMACAPRMNAEKSHNLITFIASATAP	1471
DB	236	TPYMAPEVLIOTGHSFSDADWSVCTVTEMTGAPMS--QOYKEIAFIHIGTTKSHP	293
QY	1472	SIPSHLSPGLRDVALRCLELOPQDPPSPRELLK	1504
DB	294	PIPDNISSDANDEFLKLCIQDEPNLNPRTASELLK	326
RESULT 7			
ID	022040	PRELIMINARY;	PRT; 376 AA.
AC	022040:		
DT	01-JAN-1998	(TREMBLrel. 05. Created)	
DT	01-JAN-1998	(TREMBLrel. 05. Last sequence update)	
DE	01-MAR-2002	(TREMBLrel. 20. Last annotation update)	
DE		NPRI-related protein kinase 1S.	
GN		ANP1.	
OS		Arabidopsis thaliana (Mouse-ear cress).	
OC		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
OC		eurostids I; Brassicales; Brassicaceae; Arabidopsids.	
OX		NCBI_TaxID=3702;	
RN		[1]	
RP		SEQUENCE FROM N.A.	
RC		STRAIN=COL-0;	
RX		MEDLINE=97408932; PubMed=9263451;	
RA		Nishihama R., Banno H., Kawahara E., Irie K., Machida Y.;	
RT		"Possible involvement of differential splicing in regulation of the	
RT		activity of Arabidopsis ANP1 that is related to mitogen-activated	
RT		protein kinase kinase kinases (MAPKKs).";	
RL		Plant J. 12:39-48(1997).	
CC		-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	
DR		EMBL; AB000797; BAA21855.1; -.	
DR		HSSP; P24941; IAO1.	
DR		InterPro: IPR000719; Euk_Pkinase.	
DR		InterPro: IPR002290; Ser_thr_Pkinase.	
DR		Pfam: PF00069; pkinase; 1.	
DR		ProDom: PD000001; Euk_Pkinase; 1.	
DR		SMART; SM00220; S_TKc; 1.	
DR		PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	
DR		PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
DR		PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	
DR		ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.	
SC		SEQUENCE 376 AA; 41384 MW; F23B05218673456 CRC64;	
Query Match 7.4%; Score 576; DB 10; Length 376;			
Best Local Similarity 42.3%; Pred. No. 1.le-27;			
Matches 119; Conservative 53; Mismatches 99; Indels 10; Gaps 5;			
QY	1228	PGHTAKQPIRDEDTWMLGQOIGLAFSSCYQADVDGDTLMAVQYTVRNTSSQ--E	1285
DB	57	PANVDMAP--PISWRKQGLIGRAFQTVYGMNIDSELLAVQVLIANFASKEKTQ	113
QY	1286	EVEALREIEIRMSHLNHPNIIIRMGATCEKSNYLIFFEMAGGSVAHLISYGAFFESV	1345
DB	114	AHIGLEEEVKLLKMLSHNIVRYIGTVAEDDTLMIILEFVGGSTLSLLEKFGPPPEV	173
QY	1346	VINTYEOILRGISYHENOITHRDYKANLLIDSTGQRLIADFGAARAFASLKGATGAGEF	1405
DB	174	VATYTRQLLTGLEEYLNHAIHRDIKGANIIVDNKG-CIKLADFGASKQVAELATWTG--	230
QY	1406	OGSLGTAFMAPEVLNRGOQVGRSGDWSVCCATITEMACAPRMNAEKSHNLITFIKA	1465
DB	231	AKSMGIGTYMAPEVLIOTGHSFSDADWSVCTVTEMTGAPMS--QOYKEVAAIFFTG	288
QY	1466	SATTAIPSIPSHLSPGLRDVALRCLELOPQDPPSPRELLKHP	1506
DB	289	TTKSHPIPIPDNLSSDAKDFLKCIODEVPLRLRTASELLKHP	329
RESULT 8			

[illegible]

OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-KAX-3;  
RX MEDLINE=99051319; PubMed=9832508;  
RA Chung C.Y., Reddy T.B.K., Zhou K., Firtel R.A.;  
RT "A novel, putative MEK kinase controls developmental timing and  
spatial patterning in Dictyostelium and is regulated by ubiquitin-  
mediated protein degradation.";  
RL Genes Dev. 12:3564-3578(1998).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC EMBL; AF093689; AAC97114.1; -.  
DR HSSP; P24941; 1A01.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR001810; F-box.  
DR InterPro: IPR002290; Octrept\_molif.  
DR InterPro: IPR001245; Tyr\_kinase.  
DR InterPro: IPR001680; WD40.  
DR Pfam; PF00646; F-box; 1.  
DR Pfam; PF00069; kinase; 1.  
DR Pfam; PF00400; WD40; 7.  
DR PRINTS; PRO00320; GPROTEINBRPT.  
DR PRINTS; PRO0109; TYRKINASE.  
DR ProDom; PD000001; Euk\_pkinase; 1.  
DR ProDom; PD000018; WD40; 1.  
DR SMART; SM00256; FBOX; 1.  
DR SMART; SM00016; OPR; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR SMART; SM00320; WD40; 7.  
DR PROSITE; PS50181; FBOX; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00678; WD\_REPEATS\_1; UNKNOWN\_4.  
DR PROSITE; PS50082; WD\_REPEATS\_2; 5.  
DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
KW ATP-binding; kinase; Repeat; Serine/threonine-protein kinase;  
KW Transferase; WD repeat.  
SQ SEQUENCE 942 AA; 105796 MW; C9E4928A8C7C68F7 CRC64;  
  
Query Match 7.2%; Score 562.5; DB 5; Length 942;  
Best Local Similarity 38.4%; Pred. No. 3.1e-26;  
Matches 119; Conservative 65; Mismatches 89; Indels 37; Gaps 7;  
  
QY 1212 NGEDIIIIQQDPR-----ETLRGHTKAKQPYREDTEWMLKGOQIGLGAFFSSCYQADY 1263  
DB 140 NNNNNITQHTDPSLLINEHEELNSH-----NIRKMGQILRGYGSVYLGLNK 190  
QY 1264 GTGLTAAVKQVTVYR-NTSSQEEVEVALREIRRMASHLHNPIITRMGATCEKSNYNLF 1322  
DB 191 DTGELFANQLEIVDINDPKIKNMILSFSKEIEMRSIRHNINRYRLTSLDQSLVLF 250  
QY 1333 IEMAGGSVAHLISKYGAFFKESVINTYEQLLRGLSYLHENOIIHRDYKANLLIDSTGO 1382  
DB 251 LEYIGGSISSLGKFGAFSENVIVYTKQILQGLSFLHANSIIRHDIKANILLDTKG- 309  
QY 1393 RLRIIDFGAARALASKGAGGAFGQ-----QLLGTIAFMAPEVLRGQOYGSCVWWSG 1436  
DB 310 IVKLSDFECCK-----SFGSIVQFSKSMQSTPYWMAEVIKQGHGSSDIWISIG 359  
QY 1437 CAIEMACAKPPWMAEKSHNLALIFKIASATTAPISPHLSPGLRDVALRCLTELOPODR 1496  
DB 360 CVIYEMATAQPPWS--NITELAAVNYHTIASSNSINIPSHMSQGEAFPLNLCFKDKPKER 417  
QY 1497 PPSRELLKHP 1506  
DB 418 PDANOLLKHP 427

RESULT 10  
082667 PRELIMINARY; PRI; 591 AA.  
AC 082667;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE MAP3K alpha 1 protein kinase (EC 2.7.1.37).  
GN MAP3K ALPHA 1.  
OS Brassica napus (Rape).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC Eucosids II; Brassicales; Brassicaceae; Brassica.  
OX NCBI\_TaxID=3708;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CV, TOPAS;  
RX MEDLINE=99196996; PubMed=10095117;  
RA Jouanin S., Hamal A., Leprince A.S., Tregear J.W., Kreis M.,  
RA Henry Y.;  
RT "Characterisation of novel plant genes encoding MEK/STELL and RAF-  
related protein kinases.";  
RL Gene 229:171-181(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CV, TOPAS;  
RA Jouanin S., Leprince A.S., Hamal A., Kreis M., Henry Y.;  
RT "Plant MAP kinase signalling pathways in the lme1light.";  
RL Adv. Bot. Res. 30:0-0(2000).  
DR EMBL; AJ010091; CAA08995.1; -.  
DR HSSP; P24941; ICKP.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_kinase.  
DR Pfam; PF00069; kinase; 1.  
DR ProDom; PD000001; Euk\_pkinase; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW ATP-binding; kinase; Transferase.  
SQ SEQUENCE 591 AA; 64507 MW; EAFAC591708C1FC8 CRC64;  
  
Query Match 7.1%; Score 558.5; DB 10; Length 591;  
Best Local Similarity 29.3%; Pred. No. 2.7e-26;  
Matches 149; Conservative 83; Mismatches 190; Indels 87; Gaps 14;  
  
QY 1031 RNCPPNKDSDKSPVFTOSRPLPSSNIHRPKSRPTPGNTSKQGPSKNSMTLDLNSSK 1090  
DB 7 RSSSKNKDSSL--LQOTRSYSDKSIR-----RISADNSKSSPPVYPS-----RCTPR 54  
QY 1091 CDDSFSGSSNSSNNAVIPSDEIVFTVEEKR-LDY---NTELNSSIEDLEASMP-- 1142  
DB 55 CSREFAGASGFED-----EKKCHPLPLPSLNDQVNSVSGSGSVSSG 101  
QY 1143 -----SDTVTRKSEVAYLSPEKA-----ENDDTYKDDVINNOCKEK 1181  
DB 102 SGEIOSQPTAPRKSNAALAPKAGAPTSPPLNRRSGMTLESSGTRDNGDGR----- 153  
QY 1182 EAEEREAALIAMAGSADALPIVPOLOVNGEDIIIIQQDPRFLPGHTAKQPYREDT 1241  
DB 154 -----SSEIHPLPLPGSGSPSPSVVLPCESTPSGSSGVGSSWVVGSEKELS 199  
QY 1242 EWLKGOQIGLGAFFSSCYQADYGTGLTAAVKQVTVYRNTSSQEEVEVALREIRRMASHL 1301  
DB 200 KWKGRFISGTFGKYVYOGFNEEGRICAIKEVYI-SDDKSKRCLKLOINOEIIVLSQL 258  
QY 1302 NHPNIIIRMGATCEKSNYNLFEMAGGSVAHLISKYGAFFKESVINTYEQLLRGLSYLH 1361  
DB 239 GHPNIVQYGSLSSETLSVLEFVSGSIXYKLLTEYGAFTPEVIONTRYOITLYGLAYLH 318  
QY 1362 ENQIIHRDYKANLLIDSTGO RLRIIDFGAARALASKGAGGAFGQGLGTIAFMAPEVL 1421  
DB 319 GRNIVYHRDIKGANILLVDNGE-IRLADFGMAKHVTAYST-----MLSTGSGPYWMAPEV 372



QY 1422 RG00-YGRSCDWSVGCATTEMACAPPMNAEKSNHLLALIFKATTAIPSPHLSPG 1480  
DB 373 MRRGYTLADVWVSVCCTILEMATAPKPPWS--OPEGVAALFKIGNSKDMEIPDHLSD 429  
QY 1481 LRVALRCLLEPODRPSPRELLKHPYER 1509  
DB 430 AKNFRICLQDRNPVPRPTAQLLEHPELR 458  
RESULT 11  
ID 096HN9 PRELIMINARY; PRT: 594 AA.  
AC 096HN9;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Unknown (Protein for IMAGE:3506235) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=KIDNEY;  
RA Strausberg R.;  
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC008336; AA08336.1;  
DR InterPro: IPR000719; Euk\_pkinase.  
DR Pfam: PF00069; Pkinase.1.  
DR ProDom: PD000001; Euk\_pkinase.1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
FT NON-TER 1  
SQ SQUIDNCE 594 AA; 67092 MW; P493865DB2F8C3D CRC64;  
Query Match 7.1%; Score 557.5; DB 4; Length 594;  
Best Local Similarity 31.4%; Pred. No. 3.2e-26;  
Matches 161; Conservative 78; Mismatches 173; Indels 101; Gaps 20;  
QY 1044 PVFTQSRPLPSSNIRKPKSPRPPG-----NTSKOGDPSKNSMTLDLNSSSKCDSPFG 1096  
DB 125 PPRSRHLSVSS-QNPGRSSPPGYVERQOHIAKOG-----SYT----- 164  
QY 1097 CSSSSNAVIPSDETTPPEBEKRLDYNTLNSIEDLEASPPSSDTTY---TFKSEV 1153  
DB 165 -SINSEGEIPE-----TSEQCMLDP-----LSAENSLSGSCOSLDRSADSPFRSR 212  
QY 1154 AVISPEKENDDTYKD-----DYNNHOKCKEKEAEEREE 1167  
DB 213 MSRAQSPDRKQREYSDKETQLDKGVKGGTYPRRYHVSMMHKDYSQGRKTPRIKRRHGN 272  
QY 1188 ALAI--AMAMASQDALPIVPO-----LQVNGEDIIITQDTPETLLPGHTKAKOPY 1237  
DB 273 LFTLVPSRSRLSTNGEMGLAVQYLDPRGRRLRSADSEMAISVGERNNPT-----KSP 324  
QY 1238 REDTEMLKGOQIGAGSSCQADQVGTGLMAVKQYTYVANTSSQDEVEYEALEELRM 1297  
DB 325 SAPINMRGRKLLGGAGAGRYVLCYDVTGRELASKVOQFDPD--SPETSKEVSALECEIOL 383  
QY 1298 MSHLNHNIRIIMLGATGECSENYNL--FLEWAGSVAHLISKYAPFESVYINTEOLLR 1355  
DB 384 LKNQHERIYQYQCLDRAKFKTLITFMEYIPGSSVKDQLKAYGALLESYTRKTRTQILE 443  
QY 1356 GLSLYHNEQIHRDYKCANLLIDSTGQRLRIADFGAARLAS---KGTGAEFOGOLIGT 1412  
DB 444 GMSYLSHNMIVIRDIKCANILRDSAG--NVKLGDSKRIQITCMGSG---MRSVGT 498  
QY 1413 IAPYAPVLNGOQYGRSCDWSVGCATTEMACAPPMNAEKSNHLLALIFKATTAIPSPHLS 1472  
DB 499 PYWSPSPVIGEGYGRADWVSLCTVEMTEKPPW-AEVEA--MAAIFKATIAQTPNPQ 555  
QY 1473 IPSHLSPGLRVALRCLLEPODRPSPRELLK 1505  
DB 556 LPSHISEHGRDF-LRRTFVEARQRPASBELLIH 587

RESULT 12  
ID 060030 PRELIMINARY; PRT: 1338 AA.  
AC 060030;  
DT 01-AUG-1998 (Tremblrel. 07, Created)  
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Map kinase kinase kinase.  
GN BCKL.  
OS Kluyveromyces lactic (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
OX NCBI\_Taxid=28985;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CSS2359/152;  
RX MEDLINE=99262846; PubMed=10329146;  
RA Jacoby J.J., Kirchath L., Gengenbacher U., Heinisch J.J.;  
RT "Characterization of KIBCK1, encoding a MAP kinase kinase kinase of  
Kluyveromyces lacticus".  
RL J. Mol. Biol. 288:337-352(1999).  
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AJ005079; CA006336.1;  
DR HSSP: P24941; IHCL.  
DR InterPro: IPR000886; ER\_target.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR Pfam: PF00069; Pkinase.1.  
DR ProDom: PD000001; Euk\_pkinase.1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN.1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 1338 AA; 148047 MW; BAE6B15EB7122B5 CRC64;  
Query Match 7.1%; Score 552.5; DB 3; Length 1338;  
Best Local Similarity 25.0%; Pred. No. 2.2e-25;  
Matches 211; Conservative 149; Mismatches 338; Indels 147; Gaps 32;  
QY 741 ILGNQTESNMQELLGRCLID-----RLLEFPAPFYPIVSTDV-----SQAEPE 788  
DB 535 VKSNASASNGESSDLTISDQSSHRRAVPQPSHYLYNSAEDWYFSDVET 594  
QY 789 IRYKLLSLTFALQSIDNSHSMYGLSRRIYLSARAVTVPIVFSK-LLEMLSVSSST 847  
DB 595 IS-----DAPHITLPKSRPSLKLNSVLT---HASEKSTFRRIIROTSDT 636  
QY 848 HFTMRRLMAIADEVEIAEAIOLGVEDTLDGQDSFIQAVPNPNLYETTNSSPECTVH 907  
DB 637 DIDNKRRESPPYVAELAPK-RKAPKPPVNG--NPVTSGSLPSAANVSESPLESPK 693  
QY 908 LEKTKGKL-----CATKLSA-----SEEDISERIASISVGPSSSTTTTTTTT 949  
DB 694 LDRNGKTIYQKNRPPLPPTLTERSSRSVSLSQDLNE---VKESPVGSTFPASQY 749  
QY 950 EQPKP--MOTGRPIQSCLNSSP-----LSHSQMLFPALSTP-----SSSTPS 992  
DB 750 MYPQYKALTELLPKRSADLSIRPMSLRQFSKNSLSLRKYLSTSRQTLNFTNSKPL 809  
QY 993 VPAGATVSKHRIQGFPCRIPLSPASPTQKRFSLQFHRNCPENKDSKLSLSP-----VFT 1047  
DB 810 VTSSTADIDENDISF-----ADAPELSDSDDYSAASDEIIVS 848  
QY 1048 QSRPLPSSNIRKPKSPRPPGNTSKQDPSKNSMTLDLNSSSKCDSPGSCSSNSN--- 1103  
DB 849 RDRKISINDV--PEFSFTED-----TIDLVGDTQOVSVGATGEGSDTPK 893  
QY 1104 AVISDSEVTFPVEKCLDVNTLNSIEDLEASPPSSDTTYTFKSEVAVLSPEKAE 1163

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DB 894 ALRPSDYYVYQNL-EKFFPDADLD-NPILGLTPPSPNADSSPSPRGFEKSLTKKSEQ 951
QY 1164 DDTYKDVNHNOK---CKEKMEAEELALAIAMANSASODALPIVQ-LQVEN---GE 1214
DB 952 OPATLSRGESSQFLTPVSKLPKPKTKTIRI-IAQEAERAKNEVSOKLQKNTKMGCT 1010
QY 1215 DIIIIIOQDTPETLLPGHTKAKOPYREDETEWLKGGQITGLGFSSCYQADYGTGLMAVKQY 1274
DB 1011 KVEITDKTFTISINRSNRGGEYKE-FAMIKGEITIGKSGFGAYIALANTYTGEMLAVKQY 1069
QY 1275 TVVRNTSSPOE---EVEVALREERIMSHLNHPNIIIRMLGANCEKSNVLFIEWMAGGSY 1331
DB 1070 T-VPESSODEGALISVVALKSEVSTLKDNLNHNIVQYIGFEKKNITYSLEFLEYAGGSY 1128
QY 1332 AHLKSYGAFKSSVAVINTEQLRGISYLHENQIIHRDVGANLLIDSTGQRLRIADFGA 1391
DB 1129 GSILIRYGRFPDQILRHILKQYLEGLAYLHSGILHRDKMADNLIDNDGV-CKISDFGI 1187
QY 1392 AARLASKGAGGEPGQGLGTIAFMAPEVL-RGQOYGRSCDVMSVGCALIEMACAPPMN 1450
DB 1188 SRKSNNTYNS---DNTMGTVFWMAPEMVDAHGSARVDIWSLGCYVLEMPAGRRPWS 1244
QY 1451 AEKSHNHLALIEKIASATTAAPSIPSH---LSPGLRDVALRCLEQPODRPPELKHPR 1506
DB 1245 ---NEPVVAMAFQIGKSKTAPPTPDTRKDLVSPAGSFLDQCFEIDPEMRPTASLVGHP 1301
QY 1507 VERTT 1511
DB 1302 FCKTS 1306

RESULT 13
ID 042625 PRELIMINARY; PRT; 666 AA.
AC 042625;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE MAPK kinase.
GN NRC-1.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_Taxid=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98250677; PubMed=9584090;
RA Kothe G.O., Free S.U.;
RT "The isolation and characterization of nrc-1 and nrc-2, two genes
RT encoding protein kinases that control growth and development in
RT neurospora crassa."
RL Genetics 149:117-130(1998).
CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF034090; AAC21676.1; -.
DR HSSP: P24941; 1A01.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000159; RA_domain.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR ProDom: PD000001; Euk_pkinase.1.
DR SMART: SM00220; S_TKc.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 666 AA; 73634 MW; 2BCDFCF4B98DB1F CRC64;

Query Match 6.9%; Score 542; DB 3; Length 666;
Best Local Similarity 28.6%; Pred. No. 3.4e-25;
Matches 166; Conservative 92; Mismatches 215; Indels 108; Gaps 23;
QY 1013 RIPSASP---QYGRKPSL-----QFHRNCPENKXSDK----- 1041
|:|:| | :|:| | | | | | | | | | |
```

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DB 99 RVPSGEPGAELERAAALIMEEAQOTHR--PRPESDKKSQKLQKLVLYGVGMEDLQOQPP 156
QY 1042 LSPVFTQSRPLPSSN---IHRKP---SRPPGNTSKQD-----PSKNSMTLDLNSS 1089
DB 157 LSPMSYQDERBRNVNSAARDLERAPLETPRAMPRFQALRGCGLBPSELIALSDLTSV- 215
QY 1090 KCDSDSGCSSNSNNAVPSDEYFTYVEKCRLD-VNTELN-----SSEDLEASM 1140
DB 216 -----PPDHSREAT---DRTARLSMRRSARLSRANHLSVASTLSFASISIOD--APPI 263
QY 1141 PS-SDTTFVFKSEVAALISPEKA--ENDDTYKDDVNH---NCKEKEAEELALAIAMA 1194
DB 264 PTIADSWILASNOIAKVRRDVLPRAPHGRDSVASSVTDLQEGSSPTEPNRRSRVPS 323
QY 1195 MSASODALPIV--POLQV-----ENGEDIIIOQDTPETLLPGHTKAKOPYR--- 1238
DB 324 DSGSDTAASVVIDPDGNIVRHSYSGTNMSADSVAIOELAE--DGEDAADKEIQTFLA 381
QY 1239 ---EDTEWLKGGQITGLGFSSCYQADYGTGLMAVKQYTYV-----RNTSDEEYVE 1289
DB 382 GDAMDSDMMKSKSLIGQSGFSGYIALHAITGELLAVKQVETPAPGADSKNDARKKSMTE 441
QY 1290 ALREETIRMSHNLNHPNIIIRMLGANCEKSNVNLFIEMAGSVAHLISKYAFKESYVINY 1349
DB 442 ALKREITLLRDLOHPNIVQYIGCSSAEYLNIFLEYVPGSVQTMDDYTGALPESLVRSE 501
QY 1350 TEOQLRGISYLHENQIIHRDVGANLLIDSTGQRLRIADFGAARLAS---KGTGAGEF 1405
DB 502 VHQILOGLSYVNHROIHHIDIGKANILVDNKG-TIKISDFGJSKKEALNINLGANNNH 560
QY 1406 QGQLGTIAFMAPEVLRCGOYGRSCDVMSVGCALIEMACAPPMNAEKSHNHLALIEKTA 1465
DB 561 RPSLOGSVFWMAPEMVDAHGSARVDIWSLGCYVLEMPAGRRPWS---PDCIOALAIKFI 617
QY 1466 SATTAAPSIPSHLSPGLRDVALRCLEQPODRPPELKHPR 1506
DB 618 GSKASPTIDNASEAKQFLAQTFEIDHKKRPSADEMLSP 658

RESULT 14
ID 09NYK3 PRELIMINARY; PRT; 619 AA.
AC 09NYK3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein kinase MEKK2b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang C., Lo H.;
RT "Cloning of human MEKK2 cDNA."
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF239798; AAF63496.1; -.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase.1.
DR SMART: SM00220; S_TKc.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 619 AA; 69766 MW; 242B0F562D797873 CRC64;

Query Match 6.9%; Score 539.5; DB 4; Length 619;
Best Local Similarity 29.3%; Pred. No. 4.4e-25;
Matches 178; Conservative 78; Mismatches 205; Indels 147; Gaps 22;
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Db 625 LSEBGRDVFYRKCLQJRNPNRPTTAQLDHAIVR 657

Search completed: December 20, 2002, 16:24:39  
Job time : 80 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 15:11:51 ; Search time 936 Seconds

(without alignments)  
12619.371 Million cell updates/sec

Title: US-09-697-898-1

Perfect score: 5245  
Sequence: 1 ggaataatgagcgcgcggc.....ttcaaaccaaaaaaaaaa 5245

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*  
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4564.6	87.0	4693	22	AA27079
2	4564.6	87.0	4693	23	AA168699
3	4390.6	83.7	4488	23	AA568564
4	4354	83.0	4492	23	AA568059
5	3417	65.1	5253	20	AA25072
6	3417	65.1	5253	20	AA25072
7	3387.6	64.6	5539	24	AA141578
8	3286.4	62.7	3911	20	AA25069
9	3286.4	62.7	3911	20	AA25069

10	1955.6	37.3	3260	15	AA079325	Mammalian MEK kina
11	1955.6	37.3	3260	19	AA22676	CDNA encoding a mu
12	1955.6	37.3	3260	20	AA231877	Mitogen ERK kinase
13	1955.6	37.3	3260	20	AA456619	MEK1 protein codi
14	1955.6	37.3	3260	21	AA49222	Murine MEK1 codin
15	1955.6	37.3	3260	24	AA141577	Murine MEK1-1 cod
16	1954	37.3	3260	16	AA070570	MEK1 CDNA. Mus s
17	1430	27.3	1809	23	AA249319	Human prostate exp
18	1099.2	21.0	1950	23	AA568563	DNA encoding novel
19	285.4	5.4	1693	24	AB020722	Oligonucleotide fo
20	285.4	5.4	1693	24	AB020723	Oligonucleotide fo
21	259.2	4.9	1693	24	AB020724	Oligonucleotide fo
22	259.2	4.9	1693	24	AB020725	Oligonucleotide fo
23	210	4.0	406	22	AA190875	DNA encoding novel
24	206.6	3.9	414	23	AA56058	Human polynucleot
25	195	3.7	329	23	AB07669	Human prostate exp
26	191.4	3.6	409	23	AB07668	Human prostate exp
27	190.2	3.6	223	21	AA44215	Human secreted exp
28	120.4	2.3	2073	14	AA048659	Human secreted exp
29	120.4	2.3	2527	21	AA51104	Tobacco MAP kinase
30	117.2	2.2	2193	21	AA51102	STE11 protein phos
31	112.6	2.1	1984	21	AA298321	A. thaliana MAP ki
32	112.6	2.1	2157	21	AA251103	A. thaliana gene 1
33	93.2	1.8	2155	21	AA251101	A. thaliana MAP ki
34	86.6	1.7	702	24	AB492147	Human mitogen acti
35	86.6	1.7	834	22	AA506749	Human mitogen acti
36	86.6	1.7	1896	24	AB492146	Human mitogen acti
37	86.6	1.7	2577	24	AA038849	Human kinase (PKI
38	79	1.5	5259	21	AA64328	CDNA sequence enco
39	76.8	1.5	2029	22	AA084241	Signal transductio
40	76.6	1.5	4480	23	AA519263	Human CDNA encodin
41	75.8	1.4	2503	19	AA22681	CDNA encoding a m
42	75.8	1.4	2503	20	AA231882	Mitogen ERK kinase
43	75.8	1.4	2503	21	AA49227	Murine MEK6 codin
44	75.8	1.4	2503	24	AA141580	Murine MEK2-2 cod
45	74.8	1.4	2956	22	AA094809	Human full-length

## ALIGNMENTS

RESULT 1	
ID	AA27079 standard; DNA: 4693 BP.
XX	
AC	AA27079;
XX	
DE	06-APR-2001 (first entry)
XX	
XX	Human MEK1 CDNA.
KW	Human MEK1: mitogen-activated protein kinase kinase 1;
KW	apoptosis signal regulation; programmed cell death;
KW	serine/threonine kinase; MAP kinase cascade; JNK/SAPK;
KW	Jun N-terminal kinase/stress-activated protein kinase;
KW	Bcl-2 substrate; NF-kappa-B-mediated transcription regulation;
KW	expression inhibition; antisense therapy;
KW	hyperproliferative disorder; cancer; inflammation; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	mat_peptide
FT	Location/Qualifiers
FT	1..485
FT	/*tag= a
FT	/product= "Human MEK1"
XX	
XX	US6168950-B1.
XX	
XX	02-JAN-2001.
XX	
XX	23-JUL-1999;
XX	99US-0359756.

PR 23-JUL-1999; 99US-0359756.

PA (ISIS-) ISIS PHARM INC.

PI Monla BP, Cowsert LM, Gaarde W, Ward DT;  
.....

DR WPI; 2001-122264/13.

DR P-PSDB; AAB00291.

PT New antisense compound targeting nucleic acid encoding human  
PT mitogen-activated protein kinase kinase 1 (MEK1), useful for treating  
PT diseases or conditions associated with MEK1 expression, or preventing  
PT inflammation or tumor formation -

Claim 1; Column 42-54; 35pp; English.

This sequence represents human MEK1 cDNA. MEK1 (also known as mitogen-activated protein kinase kinase kinase 1, MEK kinase 1 and MAP/ERK kinase kinase 1) is a dual-specific serine/threonine kinase which mediates cellular responses to mitogenic stimuli, being involved in JNK/SAPK (Jun N-terminal kinase/stress-activated protein kinase) MAP kinase cascades. MEK1 regulates signalling events associated with apoptosis (programmed cell death) and NF-kappa-B, both of which have been associated with the development of hyperproliferative disorders such as cancer. Specifically, MEK1 lies directly downstream of Bcl-2 in an apoptotic signalling cascade, and plays a critical role in the control of NF-kappa-B-mediated transcription at multiple points in the apoptotic cascade. The invention relates to antisense oligonucleotides targeted to the human MEK1 gene, which inhibit its expression. A series of oligonucleotides (AA227086-AA27125) were designed to target different regions of the human MEK1 RNA, and were analysed for their effect on MEK1 mRNA levels by quantitative real-time PCR. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with MEK1 expression, such as inflammation, and cancer and other hyperproliferative disorders.

SQ Sequence 4693 BP; 1340 A; 1102 C; 1143 G; 1108 T; 0 other;

Query match	87.08;	Score 4564.6;	DB 22;	Length 4693;
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Best Local Similarity 99.08; Pred. No. 0;

Matches 4647; Conservative 0; Mismatches 39; Indels 9; Gaps 5;

QY	65	CGAGCCCTGAGCAGAGCGCGCGGAGAGACCTCTCAAGGCGACAGCGCCCGCGGCTG	124
Db	2	CGAGCCCTGAGCAGAGCGCGCGGAGAGACCTCTCAAGGCGACAGCGCCCGCGGCTG	61
QY	125	CCCGGGGACTCTGTCCGGGAGCGGGCAGCGGGGGCCCGAGCGGGCGGACTGGCGGGCG	184
Db	62	CCCGGGGACTCTGTCCGGGAGCGGGCAGCGGGGGCCCGAGCGGGCGGACTGGCGGGCG	121
QY	185	GGCAGCTGCGCAAAAGTCCGGAGTGTGGAGTGTGACACAGTGGCTTGAGACACCGCTCTTCC	244
Db	122	GGCAGCTGCGCAAAAGTCCGGAGTGTGGAGTGTGACACAGTGGCTTGAGACACCGCTCTTCC	181
QY	245	TTCGCGGCTCAGCGCGGCGCTCTCTGCAGTTCCTCCCGTCCGCGGAGCCCGCGGAGCGAGCGG	304
Db	182	TTCGCGGCTCAGCGCGGCGCTCTCTGCAGTTCCTCCCGTCCGCGGAGCCCGCGGAGCGAGCGG	241
QY	305	GGAGTGGAGACGGGCTTCCAGCTCTGTGGCGGTGTCCCGCCGCCACAGACCGCCGACCGCGG	364
Db	242	GGAGTGGAGACGGGCTTCCAGCTCTGTGGCGGTGTCCCGCCGCCACAGAGCGCGCCGCGCGG	301
QY	365	GGAGCGCGCCACTTACCGAGTCTGCTGGAGCGCGCGCGGACACCGCGCGCTCGAGTCCCGGAG	424
Db	302	GGCGCGCGCCACTTACCGAGTCTGCTGGAGCGCGCGCGGACACCGCGCGCTCGAGTCCCGGAG	361
QY	425	CGGCGGAGCCGGGGGAGAAAGCGGGCGCCGCGCGAGCGCTCTCTGCAGCGCGCCCGCG	484
Db	362	CGGCGGAGCCGGGGGAGAAAGCGGGCGCCCGCGCGAGCGCTCTCTGCAGCGCGCCCGCG	421
QY	485	CCGGCTGTGAGATGAGAGATAAAGAAACTCTCAAAGGTTGGCAAGATGGATGATGTC	544
Db	422	CCGGCTGTGAGATGAGAGATAAAGAAACTCTCAAAGGTTGGCAAGATGGATGATGTC	481

OY	545	CAGAGGAAACCAATGATCAGGGAGAAATCTAGAGCAACCTGATATCCAGACCTGGAAAGACG	604
Db	482	CAGAGGAAACCAATGATCAGGGAGAAATCTAGAGCAACCTGATATCCAGACCTGGAAAGACG	541
OY	605	AATGCTTGGAAAGAGAAATATAGCGAGGGCTGTGTGTGTAAATCCAAATCCAGTTAAAG	664
Db	542	AATGCTTGGAAAGAGAAATATAGCGAGGGCTGTGTGTGTAAATCCAAATCCAGTTAAAG	601
OY	665	GAGATGGATCTGAAATGAATCACTTATAGCAGCGTGAATCTCCAGAGAGAGTCCAGCAAGT	724
Db	602	GAGATGGATCTGAAATGAATCACTTATAGCAGCGTGAATCTCCAGAGAGAGTCCAGCAAGT	661
OY	725	CGGCTTCACCAAGCTTCCAAAAGGCGCAGCATCTTCTCCAGCACTCCCATCAGTTC	784
Db	662	CGGCTTCACCAAGCTTCCAAAAGGCGCAGCATCTTCTCCAGCACTCCCATCAGTTC	721
OY	785	GCACAGTGAATCAGAAATCTCCAGAGAGTAAAGAGAAAAAGATTCCCAAGTGCCTTTTC	844
Db	722	GCACAGTGAATCAGAAATCTCCAGAGAGTAAAGAGAAAAAGATTCCCAAGTGCCTTTTC	781
OY	845	AGATGTGCAGAAATCAGACCAACCCGGAAGGCCCTTCCACAGATGGGCTTCACACATTA	904
Db	782	AGATGTGCAGAAATCAGACCAACCCGGAAGGCCCTTCCACAGATGGCTTCTCACATATA	841
OY	905	GCCTTGAGGAACAAACCGCCGTGTAAACAAATGATCGGGGCCAGACTGTACTACTGC	964
Db	842	GCCTTGAGGAACAAACCGCCGTGTAAACAAATGATCGGGGCCAGACTGTACTACTGC	901
OY	965	AGCAGATAGGGGCTTACTCTTTCTCGATTGGAGGAGACAGCCGACAAATTAATACCGG	1024
Db	902	AGCAGATAGGGGCTTACTCTTTCTCGATTGGAGGAGACAGCCGACAAATTAATACCGG	961
OY	1025	TGTTTATTTGGGCTCCAGAACTGCAGCTGTGCACGTGGAACATTTCTGTATTCATCTGCTAT	1084
Db	962	TGTTTATTTGGGCTCCAGAACTGCAGCTGTGCACAGTAATCTGTATTCATCTGCTAT	1021
OY	1085	TTTGATAGCTCCGGGTGTTCACATRGAACCTTCAGACCATGTTTATGGAGAAAATCT	1144
Db	1022	TTTGATAGCTCCGGGTGTTCACATRGAACCTTCAGACCATGTTTATGGAGAAAATCT	1081
OY	1145	TAAAGATTTTGGAGTGTGAGAGTGTTCACAAATATCAGTAAGGCTAGTCAAGGA	1204
Db	1082	TAAAGATTTTGGAGTGTGAGAGTGTTCACAAATATCAGTAAGGCTAGTCAAGGA	1141
OY	1205	TCAAAGCTCATCTGTAACACCATCCAGAAAGTTGTTTACGCGATCTCAAAATTCATATA	1264
Db	1142	TCAAAGCTCATCTGTAACACCATCCAGAAAGTTGTTTACGCGATCTCAAAATTCATATA	1201
OY	1265	CATTGTATCATCTAGTACTCTTACGTGTAGTCTGAAAGAAAGCATTAAGATGAAGAG	1324
Db	1202	CATTGTATCATCTAGTACTCTTACGTGTAGTCTGAAAGAAAGCATTAAGATGAAGAG	1261
OY	1325	ACACAGATGTGCTTATTTGCTTGTGGGATGCTTGATGAAGAAAGTCTTACAGTGTGTG	1384
Db	1262	ACACAGATGTGCTTATTTGCTTGTGGGATGCTTGATGAAGAAAGTCTTACAGTGTGTG	1321
OY	1385	AAGAGCGCTCAGAGAACAGCTGTGCACACACTGCATGTCAATTTGGCGAGAAAGTGTGA	1444
Db	1322	AAGAGCGCTCAGAGAACAGCTGTGCACACACTGCATGTCAATTTGGCGAGAAAGTGTGA	1381
OY	1445	GAAGAAATAGAGAACTTTAATATGTGCCCTTTGTAAGTCTTAAGTGAAGATCTCATGATT	1504
Db	1382	GAAGAAATAGAGAACTTTAATATGTGCCCTTTGTAAGTCTTAAGTGAAGATCTCATGATT	1441
OY	1505	TCTACAGCCAGAGTTGTCAAGTCTGTGGATTCCCTTCTTCCCTCAGAGCTGCACAG	1564
Db	1442	TCTACAGCCAGAGTTGTCAAGTCTGTGGATTCCCTTCTTCCCTCAGAGCTGCACAG	1501
OY	1565	AGCAAAACCGTACAGCAGCAGCTTTGGCTGTGATCAGCAAGAAATCAAGAGCAATTTTA	1624
Db	1502	AGCAAAACCGTACAGCAGCAGCTTTGGCTGTGATCAGCAAGAAATCAAGAGCAATTTTA	1561

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Db 1562 ACCTTACTCATATGAGAACTCAGCAATCCCTCTGCTTACAAAGATTTTACTAGCCAT 1621  
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Db 1622 GGATTTCAGGTGTTGGAATGGAATCGTTGGCTGCTTATTTTCTAGAACTGGAATGGA 1681  
QY 1745 GAGAGATGGCCCTCAGGCGTCTTCCATGATGTCAGTGGGGCCCTGCTGTTGGCAATG 1804  
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QY 1805 GGGAGACACTGGAAATTCG6GGGCGACAGTGGAGACGCCCGCAGTGGGGACCCACA 1884  
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QY 1865 GTGGGCTTCCAGACCCAGTCTCAGAGATGTTGGAGGCAATGCTGCAGCGTCTGT 1924  
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QY 1985 CCATGCTGTGTATATACCTCTTGGCCACAGTTTACGCGAAAGATCAAACTTCAGAGACTTC 2044  
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QY 2582 TTGCAATGAGATGGAATTTCCAGAGCATCAGTTGGGGGTGAAGACACTTTGATG 2641  
Db 2522 ATGCAAGATGAGATGGAATTTCCAGAGCATCAGTTGGGGGTGAAGACACTTTTACAC 2581  
QY 2642 GTCAACAGGACAGC--TTCTTTCAGGCACTGTTCCCAACAATCTGGAACACACAGA 2699  
Db 2582 GACAAACAACACAGAGCTTTTTCAGGCACTGTTCCCAACAATCTGGAACACACAGA 2641  
QY 2700 GAACAGTTCCCC--TGAGTGCACAGTCCATTTAGAGAAAACGTGAAAAGGATTAATGTGCTA 2758

Db 2642 GAACAGTTCCCC--TGAGTGCACAGTCCATTTAGAGAAAACGTGAAAAGGATTAATGTGCTA 2701  
QY 2759 CAAATTTAGTGGCAGTTTCAGAGGACATTTCTGAGAGACTGGCCAGCTTTCAGTAGGAC 2818  
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Db 2882 TTAATGTTCCAGCCCTGTGCAACCCCTTCTCTACACCCTATGTAACACTGGCACTG 2941  
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Db 2942 CAACAGATGTCCTAAGCATAGACTTCAGGATTCATTCCTCGAGAAATACCTTCGCAT 3001  
QY 3059 CTCTCAAAACACAGCGCAAGTTTCTCTACAAATTCACAGAACTGTCTGAANAACAAG 3118  
Db 3002 CTCTCAAAACACAGCGCAAGTTTCTCTACAAATTCACAGAACTGTCTGAANAACAAG 3061  
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Db 3062 ACTCAGATTAACCTTCCCACTCTTACTCAGTCAAGACCCCTGCGCCCTGTAACATAC 3121  
QY 3179 ACAGGCCAAAGCCATCTAGACCTACCCAGGTAAATACAAATTAACAGGAGATCCCTCAA 3238  
Db 3122 ACAGGCCAAAGCCATCTAGACCTACCCAGGTAAATACAAATTAACAGGAGATCCCTCAA 3181  
QY 3239 AAAATAGATACACTTATCTGAAACAGTACTTCCAAATGTGATGACAGCTTTGGCTGTA 3298  
Db 3182 AAAATAGATACACTTATCTGAAACAGTACTTCCAAATGTGATGACAGCTTTGGCTGTA 3241  
QY 3299 GCAGCAATAGTATGATTAATCTGTATACCCAGTACAGAGACAGTGTCCACCCAGTAGAG 3358  
Db 3242 GCAGCAATAGTATGATTAATCTGTATACCCAGTACAGAGACAGTGTTCACCCAGTAGAG 3301  
QY 3359 AGAAATGCAGATTAAGATGTAATACAGAGCTCAACTCCAGTATGAGACCTTCTTGAAG 3418  
Db 3302 AGAAATGCAGATTAAGATGTAATACAGAGCTCAACTCCAGTATGAGACCTTCTTGAAG 3361  
QY 3419 CATCTATGCCCTTCAAGTATACACAGTAACTTTTAAGTCAAGAGTTCCTGCTGCTC 3478  
Db 3362 CATCTATGCCCTTCAAGTATACACAGTAACTTTTAAGTCAAGAGTTCCTGCTGCTC 3421  
QY 3479 CTGAAAAGGCTGAAAATATGATATACCTTACAAAGATGATGTAATCAATAAAGTGCA 3538  
Db 3422 CTGAAAAGGCTGAAAATATGATATACCTTACAAAGATGATGTAATCAATAAAGTGCA 3481  
QY 3539 AAGAGAAATGGAAGCTGGAAGAAGAAAGCTTTAGCAATTTGCCATATGTCAGCGT 3598  
Db 3482 AAGAGAAATGGAAGCTGGAAGAAGAAAGCTTTAGCAATTTGCCATATGTCAGCGT 3541  
QY 3599 CTCAGGATGCCCTGCCCATATGTTCTGACGCTGCAGGTTGAAAATGGAAGAATATCATCA 3658  
Db 3542 CTCAGGATGCCCTGCCCATATGTTCTGACGCTGCAGGTTGAAAATGGAAGAATATCATCA 3601  
QY 3659 TTATTTCAACAGATATCACACAGACTATACAGAGCATACCAAAACCAAAACACGTTATA 3718  
Db 3602 TTATTTCAACAGATATCACACAGACTATACAGAGCATATACCAAAACCAAAACACGTTATA 3661  
QY 3719 GAGAAAGACATGTAATGCTGAAGGTCACAAGATAGGCTTGGAGCATTTTCTCTTGT 3778  
Db 3662 GAGAAAGACATGTAATGCTGAAGGTCACAAGATAGGCTTGGAGCATTTTCTCTTGT 3721  
QY 3779 ATCAGGCTCAAGATGTGGAACTGGAACCTTTAATGCTGTTTAACAGGTGACTTATGTC 3838

Db	3732	ATCAGGCTCAAGATGTGGAACTGGAACTTTAAATGGCTCTTAAACAGTGACTATGTGCA	3781
Qy	3839	GAACACATCTTCTGAGCAAGAAGATAGTACAGACCTAAGAGACAGATAGACATGA	3898
Db	3782	GAACACATCTTCTGAGCAAGAAGATAGTACAGACCTAAGAGACAGATAGACATGA	3841
Qy	3889	TGAGCCATCTGAATCATCCAAACATCATTTGATGTGGAGCCAGTGTGAAGAACA	3958
Db	3842	TGAGCCATCTGAATCATCCAAACATCATTTGATGTGGAGCCAGTGTGAAGAACA	3901
Qy	3959	ATTACAATCTCTTATTTGAATGATGGCAAGGGGATCGGTGGCTCATTTGGCTAGTAAT	4018
Db	3902	ATTACAATCTCTTATTTGAATGATGGCAAGGGGATCGGTGGCTCATTTGGCTAGTAAT	3961
Qy	4019	ATGAGCCCTTCAAGAATTCAGTAGTTATTAATACACTGACAAAGTTACTCTCGTGCCCTT	4078
Db	3962	ATGAGCCCTTCAAGAATTCAGTAGTTATTAATACACTGACAAAGTTACTCTCGTGCCCTT	4021
Qy	4079	CGTATCTCCATGAAACCAATTCATTCACAGAGATGTCAAAGTGCCAAATTTGCTAATTG	4138
Db	4022	CGTATCTCCATGAAACCAATTCATTCACAGAGATGTCAAAGTGCCAAATTTGCTAATTG	4081
Qy	4139	ACACGACTGGTCAGAGACTAAGAATTTGCAGATTTTGGACTCGACGAGTTGGCATAA	4198
Db	4082	ACAGACTGGTCAGAGACTAAGAATTTGCAGATTTTGGACTCGACGAGTTGGCATAA	4141
Qy	4199	AAGGACTGGTCAGAGAGTTTCAGGACAAATTCTGGGGCAAAATTGCATTATGCGAC	4258
Db	4142	AAGGAACTGGTCAGAGAGTTTCAGGAGCAAAATTCTGGGGCAAAATTGCATTATGCGAC	4201
Qy	4259	CTGAGGTACTAAGAGGTCACAGATATGGAAGAGCGTATATGAGAGTGTGGCTGTG	4318
Db	4202	CTGAGGTACTAAGAGGTCACAGATATGGAAGAGCGTATATGAGAGTGTGGCTGTG	4261
Qy	4319	CTATTATAGAAATGGCTTGTGCAAAAACACACAGAGAAATCAGAAAAACACTCCATATATC	4378
Db	4262	CTATTATAGAAATGGCTTGTGCAAAAACACACAGAGAAATCAGAAAAACACTCCATATATC	4321
Qy	4379	TTTGCTTTGATATTTTAAGATTGCTATGTCGAATCTCTCCATCGATCCCTTCACATTTGT	4438
Db	4332	TTTGCTTTGATATTTTAAGATTGCTATGTCGAATCTCTCCATCGATCCCTTCACATTTGT	4381
Qy	4439	CTCCGAGTTTCGAGATGTGGCTCTTGCTGTGTATTAATCTCACTCAGGACACACTC	4498
Db	4382	CTCCGAGTTTCGAGATGTGGCTCTTGCTGTGTATTAATCTCACTCAGGACACACTC	4441
Qy	4499	CATCAAGAGAGCTACTGAAAGCATCCAGTCTTTTCGTACTCATGTGAGCCAAATTATGACA	4558
Db	4442	CATCAAGAGAGCTACTGAAAGCATCCAGTCTTTTCGTACTCATGTGAGCCAAATTATGACA	4501
Qy	4559	TCAAACTACAGTAAGAACAGATGCTCAACAAGAGAAAAAACTTTGTGGGAAACCAAT	4618
Db	4502	TCAAACTAC -GTAGAAACAGATGCTCAACAAGAGAAAAAACTTTGTGGGAAACCAAT	4560
Qy	4619	GATATTTCTACGGCATGATGCCCATGTAACAGATATGAACGAGGCGAGTGGGAAACCTT	4678
Db	4561	GATAT - -CTACGGCATGATGCCCATGTAACAGATATGAACGAGGCGAGTGGGAAACCTT	4618
Qy	4679	ACCTAAGTATGTGATGACAATCATGATCTGTACCTAAAGTCAGATATGCAAAAGCCCA	4738
Db	4619	ACCTAAGTATGTGATGACAATCATGATCTGTACCTAAAGTCAGATATGCAAAAGCCCA	4678
Qy	4739	ACTAGTCAGAAACT 4753	
Db	4679	ACTAGTCAGAAACT 4693	

RESULT 2  
AAI68699  
ID AAI68699 standard; DNA; 4693 BP

AAI68699;  
AC  
XX

DT	21-JAN-2002	(first entry)
XX	Human MEK kinase MEK1 encoding DNA.	
XX	Oncogene; c-raf-1; human; MEK1; MEK kinase; raf-binding; cytosolic;	
KM	mitogen activated and extracellular stimuli regulated kinase;	
KW	gene therapy; NF-kB suppression; tumour cell proliferation;	
KW	NF-kB-mediated signal cascade; ds.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..4488
FT		/*tag= a
FT		/product= "MEK1"
FT		/partial
FT		/note= "no start codon given"
XX		
PN	WO200179501-A2.	
XX		
XX	25-OCT-2001.	
XX		
PP	17-APR-2001; 2001WO-DE01518.	
XX		
PR	14-APR-2000; 2000DE-1020138.	
XX		
PA	(RAPP/) RAPP U R.	
PA	(WIRT/) WIRTH T.	
PI	Rapp UR, Wirth T;	
XX		
DR	WPI; 2002-017617/02.	
XX	P-PSDB; AAG80184.	
PT	New nucleic acid encoding partial raf sequence, useful for identifying	
PT	compounds that block binding of raf to its activating kinase as	
PT	potential anticancer agents	
PS	Disclosure; Fig 11b-d; 66pp; German.	
XX		
CC	This invention describes a novel nucleic acid (I) that: (i) encodes at	
CC	least one raf partial sequence containing a MEK1 (mitogen activated and	
CC	extracellular stimuli regulated (MEK) kinase) binding site; (ii) encodes	
CC	at least one partial sequence of MEK1 containing a raf binding site;	
CC	(iii) is a silent mutation of (i) or (ii); or (iv) hybridizes to	
CC	(i)-(iii). The products of the invention have cytosolic activity and can	
CC	be used for gene therapy. The products also suppress NF-kB activation	
CC	resulting in inhibition of tumour cell proliferation or transformation.	
CC	(i), or proteins/peptides encoded by them, are useful for identifying	
CC	compounds that block binding of raf to MEK1. These compounds, optionally	
CC	where expressed from gene therapy vectors, are useful in human or	
CC	veterinary medicine for treatment of tumors. Antisense sequences, or	
CC	ribozymes, that bind to (i) are used to inhibit MEK1 activation. Also	
CC	nucleic acid (I') encoding at least a part of raf (or its silent	
CC	mutations or hybridizing sequences) is used to examine interaction of	
CC	encoded proteins with activation of the NF-kB-mediated signal cascade and	
CC	to screen for inhibitors of cell transformation by raf-mediated	
CC	activation of NF-kB. This sequence encodes the human MEK1 protein	
CC	described in the method of the invention.	
XX		
SO	Sequence 4693 BP; 1340 A; 1102 C; 1143 G; 1108 T; 0 other;	
	Query Match	87.0%; Score 4564.6; DB 24; Length 4693;
	Best Local Similarity	99.0%; Pred. No. 0;
	Matches 4647; Conservative	0; Mismatches 39; Indels 9; Gaps 5;
OY	65 CGAGCCCTGAGACGAGCGGCGGAGAGAGCCCTCAAGGCGAGCGCGCGGCGCTG	124
DB	2 CGAGCCCTGAGCGAGCGGCGGCGGAGAGAGCCCTCAAGGCGAGCGCGCGGCGCTG	61
OY	125 CCGCGGAGCTGCTGCGGAGAGCGGCGGCGGCGGCGGCGGCGGAGCTGCGCGCGGC	184
DB	62 CGCGGAGCTGCTGCGGAGAGCGGCGGCGGCGGCGGCGGCGGAGCTGCGCGCGGC	121



OY	185	GGCAGCTGCGCAAAAGTGCAGAGTGTGTGAGCTGGACCAGTGCCTTGAGCAGCCGCTCTTTC	244
Db	122	GGCAGCTGCGCAAAAGTGCAGAGTGTGTGAGCTGGACCAGTGCCTTGAGCAGCCGCTCTTTC	181
OY	245	TTGGCCGCTCACCGCGGGGCTCTCGACATTTCCTCGACGCTGCGGAGAGCCCGCGACGCGAGGG	304
Db	182	TTGGCCGCTCACCGCGGGGCTCTCTCCACTCTCCACTCTCCCGTGCGGAGGCCCGGGAGCGAGGG	241
OY	305	GGAGTGGGAGCAGCGCTTCCACCTCTGTGGCGGTGGCCGCGCCGACGAGAGCGCGAGCCGCG	364
Db	242	GGAATGGGAGCCGGGCTTCACAGCTGTGTGGCGGTGGCCGCGCCGACGAGAGCCCGGAGCGAGGG	301
OY	365	GGGGCGCCCACTTACCGGAGTCCGCTGGCGCGCGCCGACAGCGGGCGCTCTGAGTCCCCGAG	424
Db	302	GGGGCGCCCACTTACCGGAGTCCGCTGGCGCGCGCCGACAGCGGGCGCTCTGAGTCCCCGAG	361
OY	425	CGCGCGAGCCCGGGGAGAAACCGGGGCGCGCGCCGACGCGCTCTCTGAGCGGGCGCCG	484
Db	362	CGCGCGAGCCCGGGGAGAAACCGGGGCGCGCCGACGCGCTCTCTGAGCGGGGCGCCG	421
OY	485	CCGGTCTGAGATGAGAGATTAAGAAACTCTCAAGGGTTGCACAGATGATGATGCTC	544
Db	422	CCGGTCTCTGAGATGAGAGAAATAAGAAACTCTCAAGGGTTGCACAGATGATGATGCTC	481
OY	545	CAGAGGAACGATAGATGAGGAGAGAACTGAAAGCACTGTATTGCAGCGCTGGAAGCAGC	604
Db	482	CAGAGGAACGATATATATAGGAGAGAAACTGAAAGCACTGTATTGCAGCGCTGGAAGCAGC	541
OY	605	AATGTTTGGAAAGAGAAATAGGCGAGGGCGCTGTGGTTAAACCAATCCAGTTTAAAG	664
Db	542	AATGTTTGGAAAGAGAAATAGGCGAGGGCGCTGTGGTTAAACCAATCCAGTTTAAAG	601
OY	665	GAGATGGATCTGAAATGAATCAATCACTTTCAGAGCTGAGTCTCAGAGAGGTCGAGGCAATG	724
Db	602	GAGATGGATCTGAAATGAATCAATCACTTTCAGAGCTGAGTCTCAGAGAGGTCGAGGCAATG	661
OY	725	CGGCTTCACGAGCTTCCAAAGGGCGGAGCGCAGTCTTCTCTGGCAACTCCCATCAGGTC	784
Db	662	CGGCTTCACGAGCTTCCAAAGGGCGGAGCGCAGTCTTCTCTGGCAACTCCCATCAGGTC	721
OY	785	GCAAGTGAATTCAGAAATCTTCACAGAGTAAAGAGAAAAAGATTTTCCCAAGTGCCTTTTC	844
Db	722	GCAAGTGAATTCAGAAATCTTCACAGAGTAAAGAGAAAAAGATTTTCCCAAGTGCCTTTTC	781
OY	845	AGATGTGCAGATATACACACACCCCGAAGACCCCTTCACACAGTGGCTCTCACCATATA	904
Db	782	AGATGTGCAGATATACACACACCCCGAAGACCCCTTCACACAGTGGCTCTCACCATATA	841
OY	905	GCCCTGAGGAAACAACCGCCGTGTAAACAAATGATGGCGGCGACAGCTGATCTACTGC	964
Db	842	GCCCTGAGGAAACAACCGCCGTGTAAACAAATGATGGCGGCGACAGCTGATCTACTGC	901
OY	965	AGCAGATAGGGCCCTAATCTTTCTCTGATTTGGAGAGACAGCCCAAGCAATAATATCCGGG	1024
Db	902	AGCAGATAGGGCCCTAATCTTTCTCTGATTTGGAGAGACAGCCCAAGCAATAATATCCGGG	961
OY	1025	TGTTTATTTGGGCTCAGAACTGCGAGCTGTGCAGTGTGAACATTTCTGTATCTGCTAT	1084
Db	962	TGTTTATTTGGGCTCAGAACTGCGAGCTGTGCAGTGTGAACATTTCTGTATCTGCTAT	1021
OY	1085	TTTGATATGCTCCGGGCTTTTCAACTAGAACTTCAACACCAATGTTATTTGAGAAAAACTT	1144
Db	1022	TTTGATATGCTCCGGGCTTTTCAACTAGAACTTCAACACCAATGTTATTTGAGAAAAACTT	1081
OY	1145	TAAAGAAATTTTGAAGTTGAGAGTTTGTTCAGAGAAATATACAGTATAGCGTATGCAAGA	1204
Db	1082	TAAAGAAATTTTGAAGTTGAGAGTTTGTTCAGAGAAATATACAGTATAGCGTATGCAAGA	1141
OY	1205	TCAAAAGCTCATCTCGTAACACATCCAGAAAGTTTGTTCAGCAGTGTCAAAATTTGCATA	1264
Db	1142	TCAAAAGCTCATCTCGTAACACATCCAGAAAGTTTGTTCAGCAGTGTCAAAATTTGCATA	1201

QY	1265	CATGTCATCATCTAGTACTCTCTAGCTACTCTAGTCAGAAAACAGCATTAAGATTAAGAGC	1324
Db	1202	CATTGTCATCATCTAGTACTCTCTACATCTACTTACGAAAACAGCATTAAGATTAAGAGC	1261
QY	1325	AACACATGTCGCTCTTTGCTGTGGGCAAGCTGTGATGAAGAAAGCTTTCAGTGTGTG	1384
Db	1322	AACACATGTCGCTCTTTGCTGTGGGCAAGCTGTGATGAAGAAAGCTTTCAGTGTGTG	1321
QY	1385	AAGAGGCTGCAGGAAACAGCTGCACACCACATGTCATGTCATTTGGGCAAGAAAGTGTA	1444
Db	1322	AAGAGGCTGCAGGAAACAGCTGCACACCACATGTCATGTCATTTGGGCAAGAAAGTGTA	1381
QY	1445	GAAAGAAATAGAGAACCTTTAAATATGTCCCTTTGTAGATCTTAAGTGAGATCTCATGATT	1504
Db	1382	GAAAGAAATAGAGAACCTTTAAATATGTCCCTTTGTAGATCTTAAGTGAGATCTCATGATT	1441
QY	1505	TCTACAGCCAGAGTGTCCAAAGTCTGTGGATTCCTGATTCCTCTCTACAGCTGCACAGC	1564
Db	1442	TCTACAGCCAGAGTGTCCAAAGTCTGTGGATTCCTGATTCCTCTCTCTACAGCTGCACAGC	1501
QY	1565	AGCAAAACCGTACAGCAGCAGCCTTTGGGTGATCAGAGAGAAATCAGAGAGCAATTTTA	1624
Db	1502	AGCAAAACCGTACAGCAGCAGCCTTTGGGTGATCAGAGAGAAATCAGAGAGCAATTTTA	1561
QY	1625	ACCTTACTCATTTANGAACTACGAAATCCCTCTGCTTACAAAGATTTTACTGAGCCAT	1684
Db	1562	ACCTTACTCATTTANGAACTACGAAATCCCTCTGCTTACAAAGATTTTACTGAGCCAT	1621
QY	1685	GGATTCCAGTGTGGGATGGAACGCTGGGTGCTTTTCTTCTAGAAACGTGGAAATGGA	1744
Db	1622	GGATTCCAGTGTGGGATGGAACGCTGGGTGCTTTTCTTCTAGAAACGTGGAAATGGA	1681
QY	1745	GAGAGATGGCCCTCAGGGGCTCTTCTCCATGATGTCAGTGGGGCCCTGCTGTGGCAATG	1804
Db	1682	GAGAGATGGCCCTCAGGGGCTCTTCTCCATGATGTCAGTGGGGCCCTGCTGTGGCAATG	1741
QY	1805	GGGAGAGCATCTGGAATTTCTGGGGGACAGCAGTGAAGCAGCCCGAGTGGGGAGCCACCA	1864
Db	1742	GGGAGAGCATCTGGAATTTCTGGGGGACAGCAGTGAAGCAGCCCGAGTGGGGAGCCACCA	1801
QY	1865	GTGGGTCTTCCAGACCGATATCTCAGGAAATGTGGTGGAGGCAATGCTGCAGGCTTCTGT	1924
Db	1802	GTGGGTCTTCCAGACCGATATCTCAGGAAATGTGGTGGAGGCAATGCTGCAGGCTTCTGT	1861
QY	1925	CAATGGTCTGTCTACACCTGTCTCAAAAGTGTACGTGTGCTTTAAAAACATTGAGAG	1984
Db	1862	CAATGGTCTGTCTACACCTGTCTCAAAAGTGTACGTGTGCTTTAAAAACATTGAGAG	1921
QY	1985	CCATGCTGGTATATCTCCTTGCACACAGTTTAAAGCGAAAGATCAAACTTCAGAGACTTC	2044
Db	1922	CCATGCTGGTATATCTCCTTGCACACAGTTTAAAGCGAAAGATCAAACTTCAGAGACTTC	1981
QY	2045	TCCAGCCAGTGTAAACACATCCTAATGTCAAATGTGCGATGCCAAATAGCCGACAGTC	2104
Db	1982	TCCAGCCAGTGTGTAAACACATCCTAATGTCAAATGTGCGATGCCAAATAGCCGACAGTC	2041
QY	2105	ACGTCGTCAATCAACACACTGTGGAAAGTGTGCAAAAGGCAAGCAGAGAGATTTGGAGTGTG	2164
Db	2042	ACGTCGTCAATCAACACACTGTGGAAAGTGTGCAAAAGGCAAGCAGAGAGATTTGGAGTGTG	2101
QY	2165	GCAGAGAAATACTAAAGCTGGATTCATTTGATGTGGTGTGATTAATATCTTTAAATTT	2224
Db	2102	GCAGAGAAATACTAAAGCTGGATTCATTTGATGTGGTGTGATTAATATCTTTAAATTT	2161
QY	2225	GTAATCTTGGAAACCAAACTGAATCAAAACATTTGGCAAGAACTTTGGCCGCTTGTGC	2284
Db	2162	GTAATCTTGGAAACCAAACTGAATCAAAACATTTGGCAAGAACTTTGGCCGCTTGTGC	2221
QY	2285	TTATAGATAGACTGTGTTGGAAATTTCCGCGGAATTTTATCCATCATTTGTCAGTACTG	2344
Db	2222	TTATAGATAGACTGTGTTGGAAATTTCCGCGGAATTTTATCCATCATTTGTCAGTACTG	2281
QY	2345	ATGTTTCAACAGCTGAGCTGTTGGAATTCAGTAAACAGTAAACAGCTGCTCCCTTTAACTT	2404

2282 ATGTTTCAACAACTGAGCCTGTTGAATAGATATAGAGCTGCTCCCTTAACCT 2341  
2405 TTGCTTTGAGTCATTTGATTAATCCCACTCAATGGTTGGCAAACTTTCCAGAAAGATCT 2464  
2342 TTGCTTTGAGTCATTTGATTAATCCCACTCAATGGTTGGCAAACTTTCCAGAAAGATCT 2401  
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2642 GTCAACAGGACAGC--TTCTTCCAGGCACTGTGTTCCCAACATCTTGGAAACACAGA 2699  
2582 GACCAACACAAACAGCTTTTTCAGGCACTGTGTTCCCAACATCTTGGAAACACAGA 2641  
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2642 GACAGTTCCTCTTGAATGCACAGTCCATTTAGAGAAAAGGATTAATGGCTA 2701  
2759 CAATAATGAGTCCAGTTCAGAGCAATTTTCAGAGACTGGCCAGCATTTTCAGTAGAGC 2818  
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2819 CTTCAGTTCAGCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2878  
2762 CTTCAGTTCAGCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2821  
2879 CAATAATGAGTCCAGTTCAGAGCAATTTTCAGAGACTGGCCAGCATTTTCAGTAGAGC 2938  
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3419 CATCATGCTTCAAGTGTATACAGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 3478

3362 CATCTATGCTTCAAGTGTATACACAGTAACTTTAAGTACAGAGTGTCTGCTGCTC 3421  
3479 CTGAAAAGGCTGAAAATGATGATTAACCAAGATGATGATTAATCAAAAGTGA 3538  
3422 CTGAAAAGGCTGAAAATGATGATTAACCAAGATGATGATTAATCAAAAGTGA 3481  
3539 AAGAGAGTGAAGCTGAAAGAAAGAGCTTTTACCAATTTGCCATGCAATGTCAGCT 3598  
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3599 CTGAGATGCTCCCTCCCAATGTTCTCAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 3658  
3542 CTGAGATGCTCCCTCCCAATGTTCTCAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 3601  
3659 TTATTCACAGATACACAGAGACTCTACAGAGATACCAAGCAAAACACGCTATA 3718  
3602 TTATTCACAGATACACAGAGACTCTACAGAGATACCAAGCAAAACACGCTATA 3661  
3719 GAGAGACACTGAATGCTGAAAGGTCAACAGATAGGCTTTGGAGCATTTCTTCTGTT 3778  
3662 GAGAGACACTGAATGCTGAAAGGTCAACAGATAGGCTTTGGAGCATTTCTTCTGTT 3721  
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3722 ATCAGGCTCAAGTGTGGAGACTGAACTTTAATGGCTTTAAACAGTGAATATGCA 3781  
3839 GAAACACATCTTCTGAGCAAGAAAGATAGTAGAGCACTAAGAGAGATTAAGATGA 3898  
3782 GAAACACATCTTCTGAGCAAGAAAGATAGTAGAGCACTAAGAGAGATTAAGATGA 3841  
3899 TGAGCATCTGAATCACTCAAAACATCTTGAATGTTGGAGCCAGCTGTGAAGAGCA 3958  
3842 TGAGCATCTGAATCACTCAAAACATCTTGAATGTTGGAGCCAGCTGTGAAGAGCA 3901  
3959 ATTACATCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4018  
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4259 CTGAGGATTAAGAGGTCAACAGTATGAAGAGGTGATGATGATGATGATGATGATGATG 4318  
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4319 CTATTAAGAAATGCTTGTGCAAAACCAATGGAATGCAAAACCAATGGAATGGAATGGA 4378  
4262 CTATTAAGAAATGCTTGTGCAAAACCAATGGAATGCAAAACCAATGGAATGGAATGGA 4321  
4379 TTGCTTTGATTAATTAAGATTTGATGCAACTACTGCTCATGATCCCTTCAATTTGT 4438  
4322 TTGCTTTGATTAATTAAGATTTGATGCAACTACTGCTCATGATCCCTTCAATTTGT 4381  
4439 CTCTGCTTTTACAGAGTGTGCTCTTCTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4498  
4382 CTCTGCTTTTACAGAGTGTGCTCTTCTGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4441  
4499 CATCAAGAGGTACTGAAGGATCAAGTCTTCTGATCAATGATGATGATGATGATGATGATG 4558  
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Db 902 AGCAGATAGGCGCTAATCTTTCTGATTTGGAGACACAGCCAGACAAATTAATACC6G 961  
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Db 3062 ACTCAGATTAACCTTCCCAAGTCTTACTCAGTCAAGACCTTGGCCCTCAGTAATATAC 3121



CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX

Sequence 4492 BP: 1266 A; 1057 C; 1101 G; 1067 T; 1 other:

Query Match 83.0%; Score 4354; DB 23; Length 4492;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 4445; Conservative 0; Mismatches 36; Indels 10; Gaps 6;

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QY 125 CGCGGAGACTGCTGGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 184  
DB 62 CGCGGAGACTGCTGGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 121  
QY 185 GCGAGCTGCGCAAAAGTGCAGAGTGTGAGCTGAGCAGCTGCTGAGCAGCGCTCTCC 244  
DB 122 GCGAGCTGCGCAAAAGTGCAGAGTGTGAGCTGAGCAGCTGCTGAGCAGCGCTCTCC 181  
QY 245 TTGCGCCTCAGCGCGCGCTCTGCACTTCCCGTGCAGGAGCGCGGAGCGAGCGG 304  
DB 182 TTGCGCCTCAGCGCGCGCTCTGCACTTCCCGTGCAGGAGCGCGGAGCGAGCGG 241  
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QY 365 GCGGCGCGCGCGCTTACCGAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGG 424  
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QY 425 CGCGCGAGCGCGGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 484  
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DB 422 CGGCTGTGAGATGGAATTAAGAACTCTCAAGGGTTGCAAGAGATGATGCTG 481  
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Db 4142 AAGGAATGTGTGAGAGAGTTTCAAGGACAAATTTCTGGGCAAAATTTAATGGAC 4201
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QY	946	CCGACGACTGTA	CTTACTG	CAGCGAGAT	AGGCGCT	AACTCTTTCTTGAT	TGGAGAGAC	AGC	1003
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QY	1006	CCACACAT	TAATAAT	CCGGGGT	TTAT	TGGGCC	CACAACTG	AGCGTGCAC	1065
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QY	1066	TTCTGTAT	TATCAT	CTGCAAT	TTTGAT	GTCTCCGGGT	TTTCAACT	TGAACCTTCAC	1125
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QY	1126	ATGTAT	TATGAG	AAAAA	ACTTT	TAAGAAT	TTT	TGAGATTG	1185
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QY	1306	AGCAT	TAAGA	GATGA	AGAGAA	CAGATGT	CTTAT	TGCTTGTGGCAT	1365
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QY	1366	GAAAGT	CTTAC	AGTGT	TGA	AGACGGCT	GCAGAA	CAACACTG	1423
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QY	1426	ATTGTC	CAGACAA	AGATTA	ATAA	AAATAT	AGAACTTT	TAATATG	1485
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Db	1479	AAGTGA	AGATCT	CA	TGAATTT	CTACAG	CCAGAT	GTGTCAAGT	1538
QY	1546	TCCCTC	AGAGCT	GCACAG	CAGAA	CCGT	TACAG	CACACTTT	1602
Db	1539	TCCCTC	AGAGCT	GCACAG	CAGAA	CCGT	TACAG	CACACTTT	1598
QY	1603	AGGAAT	CAGAGAC	CAATTT	TAACT	TACTCAT	TAT	TAGAACA	1662
Db	1599	AGGAAT	CAGAGAC	CAATTT	TAACT	TACTCAT	TAT	TAGAACA	1655
QY	1663	TACAA	AGATTT	AGCTGA	GCAGCAT	GATTCAG	GT	TGGAATG	1722
Db	1659	TACAA	AGATTT	AGCTGA	GCAGCAT	GATTCAG	GT	TGGAATG	1718
QY	1723	TTTTCT	TAGAA	CT	TGGAAT	GTGAAGAGAT	TG	GGCCTT	1782
Db	1719	TTTTCT	TAGAA	CT	TGGAAT	GTGAAGAGAT	TG	GGCCTT	1778
QY	1783	GGGGCC	CGTGT	GGGAAAT	TGGGGAG	AGCACTG	GGAAAT	TTTGGGGG	1842
Db	1779	GGGGCC	CGTGT	GGGAAAT	TGGGGAG	AGCACTG	GGAAAT	TTTGGGGG	1838
QY	1843	AGCCG	AGTGGGG	AGCCAC	ACAGT	GGGTCTTCC	CAGAC	CAAGTAT	1902
Db	1839	AGCTTA	AGCGGGG	AGCGGAG	CGGAGG	GTCTTCC	CACAG	CCAGAT	1896
QY	1903	GAGC	ATGCTG	CACGCTT	CTCA	TGATGTGT	GTGTG	CTGACCTG	1962
Db	1899	GAGC	ATGCTG	CACGCTT	CTCA	TGATGTGTGT	GTGTG	CTGACCTG	1958
QY	1963	GCTG	CTTTAAAA	AATG	TGAGAG	CAATGCTG	TAT	TATAGCTT	2022
Db	1959	GCTG	CTTTAAAA	AATG	TGAGAG	CAATGCTG	TAT	TATAGCTT	2018
QY	2023	AGAA	TCAAAC	CTTC	GAGAC	CTTCC	ACAGC	AGTTGT	2082

[illegible]



FT 3'UTR 4497..5253  
FT mat-peptide /\*\*tag= C  
FT 2637..4493 /\*\*tag= d  
FT /note= "Active fragment that mediates apoptosis"  
XX W09941385-A1.  
XX  
XX 19-AUG-1999.  
XX  
XX 12-FEB-1999; 99MO-US02974.  
XX PF  
XX 13-FEB-1998; 98US-0023130.  
XX PR  
XX (CADU-) CADUS PHARM CORP.  
XX PA  
XX Johnson GL;  
XX  
XX WPI: 1999-508649/42.  
XX P-PSDB: AAY26234.  
DR  
DR A new mammalian serine-threonine protein kinase for treating  
PT disorder characterized by aberration of the enzyme gene  
PT  
XX  
PS Claim 1a: Page 113-119; 149pp; English.  
XX  
XX The present sequence is an isolated murine MEK1 cDNA. It encodes  
CC Mitogen ERK kinase kinase 1 (MEK1) protein, which functions to  
CC integrate proteases and signal transduction pathways involved in the  
CC regulation of apoptosis. It is a 196 kDa protein kinase, which upon  
CC cleavage at Asp 871/874 by caspase generates a 91 kDa kinase fragment  
CC that induces apoptosis and a 113 kDa NH2-terminal fragment. Mutant MEK1  
CC proteins that are resistant to cleavage by caspase proteases and capable  
CC of inhibiting apoptosis can be produced. MEK1 proteins and antibodies  
CC immunoreactive with MEK1 are used in diagnostic and therapeutic  
CC assays and reagents for detecting and treating disorders involving  
CC aberrant expression or activation of the MEK1 gene products. DNA probes  
CC or primers that selectively hybridise to MEK1 cDNA, can be used for its  
CC detection in samples.  
XX  
SQ Sequence 5253 BP; 1299 A; 1403 C; 1433 G; 1118 T; 0 other;  
Query Match 65.1%; Score 3417; DB 20; Length 5253;  
Best Local Similarity 83.5%; Pred. No. 0;  
Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;  
QY 1 GAGAAATGCGCGCGCGGGAATCGCCTGTCGTGGGATTCCCGGCGCAGG 60  
DB 9 GAGAAATGCGCGCGCGGCGGATCGCCTGTCGTGGGATTCCCGGCGCAGG 68  
QY 61 GCTACGAGCCCTGAGCGAGCGCGGCGC-----GGAGAGCCCTCAAGCGAGCAGC 111  
DB 69 GCGCGCGAGTCGCGCGCGCGCGCGCGCGAGAGAGGAGGAGCTCCAGGAGCGCGC 128  
QY 112 GCGCGC---GCGGCTGGCGCGGAGCTGTCGCGGAGCGCGCGCGCGCGGAGG 168  
DB 129 GCGCGCGCGAGCGCGCGCGCGCGGCTGTCGCGGAGCCTGCGAGCGCGCGGAGGCGC 188  
QY 169 GCGGACTGGCGCGCGCGAGCTGCGCAAAAGTGGAGTGGAGCTTGAGCAGCTGCT 228  
DB 189 GCGGACTGGCGCGCGCGCGAGCTGCGCAAAAGTGGAGTGGAGCTTGAGCAGCTGCGC 248  
QY 229 GAGCAGCCGCTCTCTCTGCGCGCTCAACCGCGGCT---CCTGAGCTTCCCGTGGCG 285  
DB 249 GAGCAGCCGCTCTCTCTGCGCGCGCGCTGCGCGCGCTGCGCCTGCTGCTGCGCG 308  
QY 286 GAGCGCGCGGAGCGAGGAGGAGTGGAGCGGCTTCCAGCTGAGGCGGCGCGCGCGCGC 345  
DB 309 GAGCGCGCGGAGCGGCTGCGAGGAGGAGTGGCTTCCAGCGCGCGCGGAGCGCGCAGCC 368  
QY 346 CAGCGAGCGCGAGC 405  
DB 369 CCGGAGCGCGGAGCTCGCTGGGCTCCACCTCTCCGAGCTGGGCGCGCGCGCGGAGCAGC 428

QY 406 GCGCGCTGAGTCCCGCAGCGCGCGAGCGCGGAGAAAGCGGCGCGCGCGCGAGCGC 465  
DB 429 GCGCGCGCGAGCGCGCGCGG-----GCGGAGCGC 458  
QY 466 TCTCTGCGAGGCGCGCGCGCGGTCGTGAGATGGAATTAAGAACTCTCAAGAGTGTG 525  
DB 459 CCTCTGCGAGGCGCGCGCGCGCGGTCGAGATGGAATTAAGAACTCTCAAGAGTGTG 518  
QY 526 CACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 585  
DB 519 CACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 578  
QY 586 ATGCCAGCTGGAAGCAGCAATGTTGGAAGAGAGAAATAGCGAGGCTGTGTGTGTA 645  
DB 579 ATGCCAGCTGGAAGCAGCAATGTTGGAAGAGAGAAATAGCGAGGCTGTGTGTGTG 638  
QY 646 AAACCAATCCCAATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 705  
DB 639 AAGCCATCTTATTAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 698  
QY 706 GAGAGCTCCAGCGCAAGTGGCGCTTCCAGCAGCTTCCAAAGCGCGAGCTCTCTCT 765  
DB 699 GAGAGGCGCGAGCGAGTTCGCTGACACAGCGCGCGCGCGCGCGCGCGCGCGCGCGC 758  
QY 766 GCGAATCCCGCATGAGTGCAGCAGTGAATCAGATCTCCAGAGTAAAGAGAGAGAGAG 825  
DB 759 GCGAGCTCTCGTACAGCGCGCTCGGTGAAGCGGAAATCCAGAGAGTAAAGCGAGAG 818  
QY 826 GTTTCGCCAGTGGCTTTTCAGAGTGGAGATACACACCGCGAGAGCGCGCGCTTACCA 885  
DB 819 GTTTCGCCAGTGGCTTTTCAGAGTGGAGATACACACCGCGAGAGCGCGCGCGCGCGC 878  
QY 886 GATGCGCTTCCAT 945  
DB 879 GATGCGCTTCCAT 938  
QY 946 GCCAGCTGATCTACTGACAGCAGATAGGCGCTTAACTTTCTGATTTGAGAGAGACAGC 1005  
DB 939 GCCAGCTGATCTACTGACAGCAGATAGGCGCTTAACTTTCTGATTTGAGAGAGACAGT 998  
QY 1006 CCAGCAATTAAT 1065  
DB 999 CCAGCAATTAAT 1058  
QY 1066 TTTCTGATTTCACTGCTATTTGATGCTCCGCGGCTTCAACTTGAACCTTCAAGACCA 1125  
DB 1059 TTTCTGATTTCACTGCTATTTGATGCTCCGCGGCTTCAACTTGAACCTTCAAGACCA 1118  
QY 1126 ATGTTATGAG 1185  
DB 1119 ATGTTATGAG 1178  
QY 1186 AGTAGGCTGATCTCAAGAGATCAAGCTCACTCTGATACACATCAAGAGAGAGAGAG 1245  
DB 1179 AGTAGGCTGATCTCAAGAGATCAAGCTCACTCTGATACACATCAAGAGAGAGAGAG 1238  
QY 1246 CGCATGTCATTAATTTCAAT 1305  
DB 1239 CGCATGTCATTAATTTCAAT 1298  
QY 1306 AGCATTAAGAGATGAAG 1365  
DB 1299 AGCATTAAGAGATGAAG 1358  
QY 1366 GAAAGCTTCAAGTGTGAAG 1425  
DB 1359 GAAAGCTTCAAGTGTGAAG 1418  
QY 1426 ATTTGGCGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1485  
DB 1419 ATTTGGCGAGAGAGATGAG 1478

QY	1466	AAGTGGAGATCTCATGATTTTCTTCTACAGCCACAGAGTTGTCAAGTCTCTGTGATTTCCCTTCT	1543
Db	1479	AAGTGGAGATCCCATGTGACTTCTACAGCAAGATTTATCAAGCCCGGTGGAGTCCCGCC	1538
QY	1546	TCCCTCAGAGCTGCACAGCAGCAACCGGTACACAGCAGCCTTTGGTGGAGTCA --- CGA	16020
Db	1559	TCCCTGGAGAGCTGTCCACAGCCATCTCCCGCAGACCCCGTGGCCGGATTCACAGCG	15989
QY	1603	AGGAATCAAGAGACAAATTTTAACCTTACTCATATATGAAATCAGCAAAATCCCTCTGCT	1662
Db	1599	AGGAATCAGAGAGACAGTTTAACTTACTCATATTTGGAAACCAAGATTTCTTCCGCT	1658
QY	1663	TACAAAGATTTAGCTGAGCCATGATTCAGGTTTTGGAAATGGAATCGTTGGCTGCTTA	17222
Db	1659	TACAAAGATTTGGCCGAGCCATGATTCAGGTTTTGGAAATGGAATCGTTGGCTGCTTA	1718
QY	1723	TTTTCTAGAAACTGGATGTGAGAGAGATGGCCCTCAGCGTCTTCCCATATGTCAGT	1782
Db	1719	TTTCTTAGAAACTGGAACTGTAAGGAAATAGGCCCTTAGCGTCTTTCCACAGACGTTAGT	17787
QY	1783	GGGGCCCTGCTGTTGGCAAAATGGGGAGACATGAAATTTCTGGGGCGAGCAGTGGAAAC	1842
Db	1779	GGGGCCCTGCTGTTGGCAAAACGGGGAGAGACATGAAACTCTGGAGGGCGAGTGGGGC	1838
QY	1843	AGCCCAAGTGGGGAGCCACCACTAGGGGTCTTCCCAACACAGTATCTCAGAGAGATGGTG	1902
Db	1839	AGCTTAAACGGGGAGGGGACCGGGGTCTCTCCACCCAGCATCTCAGGGGATTTGGTG	1898
QY	1903	GAGCAGATCTCAGCAGTCTCTGTCATATGGTGTGTGCTGAGCCCTGTGTACAAATGTAGCTT	1962
Db	1899	CAGCGCTGTCTCAGTGTCTCTGTATATGTGTGGCGCTGACCCCTGTCTACAAATGTAGCTT	1958
QY	1963	GCTGCTTTAAAAACATTTGAGAGCCATGCTGTGTATATCTCTTGGCACAGTTTACGGAA	20222
Db	1959	GCTGCTTTAAAAACATTTGAGAGCCATGCTGTGTATATCTCTTGGCACAGTCTGGCAGAA	2018
QY	2023	AGAAATCAAACTTCAGAGACACTTCTCCACGCCAGTTGTAGAACATCTCTAGTCAATGTGCA	2082
Db	2019	AGAAATCAAACTTCAGAGACACTTCTCCGCCAGTTGTAGAACATCTCTGTCTCAAGTGTCA	20787
QY	2083	GATGCCAATATGCCACACAGTCTCAGCTGTCCATATCAACCTGTGGAACTGTGCCAAAGGC	2142
Db	2079	GATGCCAACAGCCGCGACAGATCAGCTGTCCATATCTACAGTCTGGAACTGTGCCAAGGC	2138
QY	2143	CAAGCAGAGAGTTGGCAGTTGGCAGAGAAATCTAAAGCTGGATCCATTTGTTTGGT	2202
Db	2139	CAAGCAGAGAGAGTTGGCGGTTGGGAGAGAAATCTAAAGCTGGGTCATCGGGGTTGGT	2198
QY	2203	GGTGTGATTTATGTCTTAAATTTGTATTTCTTGGAAACCAACATGCAATCAATTTGGCA	2262
Db	2199	GGTGTGATTTATGTCTTAAATTTGTATTTCTTGGAAACCAACATGCAATCAACATTTGGCA	2258
QY	2263	GAACTCTTGGCGCCCTTGTCTTATATAGATAGATCTTTTGGAAATTCCTGCTGAATTT	2322
Db	2259	GAACTCTGGGTGGCCCTGTCTTATATAGACAGGTTCTCTTGGAAATTCCTGCTGAATTC	2318
QY	2323	TATCCTCATATTTGTCACTAGTGTATGTTTCCACAGCTGAGCCTGTGGAATCAGGTATAG	2382
Db	2319	TATCCTCATATTTGTCACTAGTGTATGTTTCCACAGCTGAGCCTGTGGAATCAGGTATAG	2378
QY	2383	AAGCTGTGTCCCTCTTAAACCTTTGCTTTTGCGTAGTCCATTTGAATTTCCCATCAATGGTT	2442
Db	2379	AAGCTGTGTCCCTCTTAAACCTTTGCTTTTGCGTAGTCCATTTGAATTTCCCATCAATGGTT	2438
QY	2443	GGCAAACTTCCACAGAGATCTCTTGAAGTGTGGCAAGAAATGGTATCTACAGTACCCTAT	2502
Db	2439	GGCAAGCTCTCCGAGAGATATATCTAGCTCTGCGCAGGATGTGATCCGCAAGTGGCCCT	2498
QY	2503	GTTGTTTCAAAAAGCTTAGAGAAATGTGAGTGTTCAGTTCCACTCATTCCACAGAGATG	2562
Db	2499	GTTGTTTCCAAAGCTGTGTAACAGATGCTTAAATGCTTGTGGCTCCACCCACTTACACAGATG	2558
QY	2563	CTGTCCGCTTTGATGCTATTTGACAGATAGAGTGGAAATTTGCCGAAGCATCCAGTTGGGC	2622

Db	2559	CGCCGGCCCTCGAATGGCGTATCCGGAGTAGAGTGAAGAAATTCGGAGGTCTATCCAGCTGGGT	2618
Qy	2623	GTAGAGACACATTTTGATGGTGCACACAGACAGCTTCTTGACAGGACATCTTCCCAACAC	2682
Db	2619	GTGGAGGACACTGTGGATGGGCATCAGGACAG--CTTACAGGCCGTGGCCCCACCGC	2675
Qy	2683	TATCTGGAAACACAGAGAACAGTTCCTCCCTGAGTGGCACAGTCCATTTTAGAGAAACTGGA	2742
Db	2676	TGCTC-----AGAAAAAGCTCCCTTGAGCACACAGTCCATAGAGAGAAACTGGA	2726
Qy	2743	AAAGCATTTATGCTTACAAAAATTGAGTGCACGTTTCAGAGACATTTCTGAGAGACTGGCC	2802
Db	2727	AAAGGACTAAATGGTATGAGAGACTGAGTGCAGCTCGGAGAGACATTTCTGACAGACTGGCC	2786
Qy	2803	AGCATTTAGTAGAGACCTTCGTAGTTCAACAAACAACAACAACAACAACAACAACAACA	2862
Db	2787	GGCGTCTGTAGAGACTTCCAGCT-----CAACACACACAGACACACCA	2831
Qy	2863	AAGCCATGATGTTCAACAAAAAGGACGCCACAGTCAGTGTGTTGAACTCCTCTCTTA	2922
Db	2832	AAGCCAGGAGTTTCAACAAAAAGGACGCCACACAGTCAGTGTGAACTCCTCTCTTG	2891
Qy	2923	TCTCATTTTCCCAATTAATGTTTCCAGCCTTGTCAACCCCTTCTTCTTAACCCATCT	2982
Db	2892	TC--TCATGCTCAATTAATGTTTCCAGCACATCAGCCCTGTGTCCTTCGCCCTCT	2948
Qy	2983	GTACCAAGCTGGCACTGCACAGATGTCCTAACACATAGACTTCAGGAGTTATCTCCGCG	3042
Db	2949	GTCC-----CAGATATTTCTTAACACACAGACCCAGGACATTTGTTCCCTGC	2993
Qy	3043	AGAAATACCTTCTGCATCTCTCAACACACAGCGCAAGTTTCTCAATTCACAGAAAC	3102
Db	2994	AAAAATACCTTCGGATCTCCTCAGACACAGCGCAAGTTCTCTCAATTCACAGGAAC	3053
Qy	3103	TGTCCTGAAAACAAAGACTCAGATAACTTTCCCACTCTTACTAGTCAAGACCCCTTG	3162
Db	3054	TGCTCTGAAACACCAAGACTCAGACACAGCTCTCCCACTCTTCACTCAGTCAAGACCCCA	3113
Qy	3163	CCCTCAGTACATACACAGAGCCCAAGGCCATCTAGACCTACCCCGAGTATCAAGTAAA	3222
Db	3114	CCCTCAGTAAACATACACAGAGCCCAAGGCCATCTCCGACCCGTTCCGGGAGTACAAAGCAA	3173
Qy	3223	CAGGAGATCCCTCAAAAAATAGCATGACACTTGATCTGAACAGTAGTTCCCAATGTGAT	3282
Db	3174	CTAGGGGAGCGCACAAAAAGTAGATGACACTTGATCTGGGACAGTGTCCAGGTGTAC	3233
Qy	3283	GACAGCTTGGCTGTACAGCAATAGTAGTAATGCTGTTATACCCAGTACAGACAGCTG	3342
Db	3234	GACACCTTTGGCGGCGGCGGCAACAGTGGCAACGCCGTATACCCAGGACAGACAGCTG	3293
Qy	3343	TTCAACCCAGTAGAGGAGAAATGAGATTGATGTCAATACAGAGGTCAACTCCAGTATT	3402
Db	3294	TTCAACGCGGAGTGGAGGACAAAGTGCAGTTTAGATGTAAACACCGAGGTCAACTCCAGCTAC	3353
Qy	3403	GAGGACCTTCTTGAAGCATATAGCTCTCAAGTAGATACAACAGTAACCTTTAAAGTCAGAA	3462
Db	3354	GAGGACCTTCTTGAAGCATCATGCTCTCAAGTAGACACAGCATCACTTCAAGTCCGAA	3413
Qy	3463	GTTGCTGTCTGTCTCTCTGAAAAAGCTGAAAAATGATGATACCTACAAAGATGATGAT	3522
Db	3414	GTCCGCGTCTCTCTCTCCGAAAAAGGCGGAAAAATGAGACACCTACAAAGACAGCTCAAT	3473
Qy	3523	CATATATCAAAAGTCAAGAAAGAAAGTAGGAAAGCTGAAAGAAAGAAAGCTTTAGCAATTGCC	3582
Db	3474	CATATATCAAAAGTCAAGAAAGAAAGTAGGAAAGCTGAAAGAAAGAAAGCTTTAGCGATGCC	3533
Qy	3583	ATGGCAATGTACGGTCTCAGAGATGCCCTCCCATAGTTCTCAGCTGAGAGGTTAAAT	3642
Db	3534	ATGGCGATGTACGGTCTCAGAGATGCCCTCCCATGTGCTCCAGCTGAGGTGAAAT	3593
Qy	3643	GGAGAGATATCATTTATTTCAACAGGATACACGAGACCTTACACGAGATACCAA	3702

Db 3594 GGAGAGATATTTTCATTCATTCAGCAGACACACCAACCACTCTTCCAGCATACCAAA 3653  
Qy 3703 GCAAAACACCCCTATAGAGAGACACTGAATGGCTGAAAGGTCAACAGATAGGCTTGA 3762  
Db 3654 GCGAAACAGCCTTACAGAGAGAGCGGTGAGTGGCTGAAAGCCAGCAGATAGGCTCGGA 3713  
Qy 3763 GCATTTTCTTCTTGTATATCAGGCTCAAGATGGGGAACGTGAACCTTAAATGGCTTTAAA 3822  
Db 3714 GCATTTTCTTCTTGTATATCAGGCTCAAGATGGGGAACGTGAACCTTAAATGGCTTTAAA 3773  
Qy 3823 CAGTGCATATGTGCAAGAACACATCTTTCAGACCAAGAGATAGAGCACTAGA 3882  
Db 3774 CAGTGCATATGTGCAAGAACACATCTTTCAGACCAAGAGATAGAGCACTAGA 3833  
Qy 3883 GAAGAGATTAAGATATGATGAGCCTATCTGATCAACCAATCATTTAGATGGGAGCC 3942  
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Qy 3943 ACCTGTGAGAGAGCAATTAACAATCTCTTCATTTGATGATGAGGAGGAGATCGTGCT 4002  
Db 3894 ACCTGTGAGAGAGCAATTAACAATCTCTTCATTTGATGATGAGGAGGAGATCGTGCT 3953  
Qy 4003 CATTTGCTGATTAATATGAGCCTTCAAGAAATCAGTATTAATTAATCTACATGAGACG 4062  
Db 3954 CACCTCTTGAGTAAATAGGAGCTTTCAGAGACAGTCTCATTAATCACTACATGAGACG 4013  
Qy 4063 TTACTCGTGAGCCTTTCATCTCATGAAACCAATCATTCACAGAGATGTCAAAGT 4122  
Db 4014 TTACTCGTGAGCCTTTCATCTCATGAAACCAATCATTCACAGAGATGTCAAAGT 4073  
Qy 4123 GCCAATTTGCTAAATGACAGCAGCTGTGACAGACTTAAGAAATTTGCAATTTTGAGCTGCA 4182  
Db 4074 GCCAATTTGCTAAATGACAGCAGCTGTGACAGACTTAAGAAATTTGCAATTTTGAGCTGCT 4133  
Qy 4183 GCCAGGTGGCATCAAAAGAGACCTGGGAGAGAGTTTGAAGGAGCAATTAAGTGGGAGCA 4242  
Db 4134 GCCAGGTGGCATCAAAAGAGACCTGGGAGAGAGTTTGAAGGAGCAATTAAGTGGGAGCA 4193  
Qy 4243 ATTGCATTTATGACAGCTGAGTACTTAAGAGGTCAACAGATAGGAGAGCTGTGATGA 4302  
Db 4194 ATTGCATTTATGACAGCTGAGTACTTAAGAGGTCAACAGATAGGAGAGCTGTGATGA 4253  
Qy 4303 TGGAGTGTGGCTGTGCTATTAAGAAATGGCTTTGCAAAACCCAGCATGAGATGCAAA 4362  
Db 4254 TGGAGTGTGGCTGTGCTATTAAGAAATGGCTTTGCAAAACCCAGCATGAGATGCAAA 4313  
Qy 4363 AAACAGTCCCAATATCTGCTTGAATTTAAGATGCTGATGCAATCTGCTCCATCG 4422  
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Qy 4423 ATCCCTTCACATTTGCTCTGCTTTCAGAGATGGGCTCTGCTTTTGAAGACTTCAA 4482  
Db 4374 ATCCCTTCACACCTGCTCCGAGGCTGCGAGAGTGGGCTGCGCTCTTAAGAACTTCA 4433  
Qy 4483 CCTCAGAGACAGCCTCATCAAGAGACTACTGAGCATCCAGTCTTTCGTAATCAATG 4542  
Db 4434 CCTCAGAGACAGCCTCATCAAGAGACTACTGAGCATCCAGTCTTTCGTAATCAATG 4493  
Qy 4543 TAGCAATTTGAGATCAATCAATAGTAAAGAACAGATGCTCAACAAAGAAAAAAACT 4602  
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Qy 4603 TG----TGAGGAACACATTTGATTTCTACTGGCATGATGCACTAAGAGATAGAC 4658  
Db 4554 AGAACTTGTGGGGAGACATCCGCTAACGCGACGCCCTCAAGCCATCAAGCAAGAAAC 4613  
Qy 4659 GAGGCCAGTGGGGAACCCCTTACTAAGTATGATGATGACAAATCAGATCTGATCTAAG 4718  
Db 4614 GGGGCGCGCGGGGAA--CCGTAACCTAAGCATGTGATTAACAATATCAGCTGTACTAAG 4672  
Qy 4719 CTCAGTATGCA--AAAGCCAAAGTATGAGAAACCTTAACGTGTGCTTTCAAGAACT 4777  
Db 4673 CTCGATATGCAACATCTACAGCTCGTGCAGAGACTGCACACCGTCTTTCACAGAGACT 4732

Qy 4778 GGCCTAGGTGAACAGGAAAAACATGAGTTCGATGATTAATTTGCAAGCATTAATTT 4837  
Db 4733 GGCTCTGGGGGACACGAGAGCGCATGTGATGATCACTAAAGAACAGCATTAATTT 4792  
Qy 4838 TATTTTGTGAGCAGCTTTTTCAGCAA 4864  
Db 4793 TA--TTTGTGAGCAGCTTTTTCAGCTA 4817  
RESULT 7  
AAL41578  
ID AAL41578 standard; cDNA; 5539 BP.  
XX  
AC AAL41578;  
XX  
DT 19-APR-2002 (first entry)  
XX  
DE Murine MEK1-2 coding sequence.  
XX  
KW Mouse; MEK1; mitogen ERK kinase; enzyme; cancer; neuroprotective;  
KW autoimmune disease; signal transduction; allergy; inflammation;  
KW neurological disorder; hormone-related disease; apoptosis; infection;  
KW cytostatic; immunosuppressive; antiinflammatory; antiallergic; gene;  
KW neotropic; antiparkinsonian; contraceptive; ss.  
XX  
Mus musculus.  
XX  
OS  
XX  
FH Key Location/Qualifiers  
FT CDS 1..4782  
FT /tag= a  
FT /product= "MEK1.2"  
PN US6333170-B1.  
XX  
PD 25-DEC-2001.  
XX  
PE 05-APR-1996; 96US-0628829.  
XX  
PR 15-APR-1993; 93US-0049254.  
PR 14-OCT-1994; 94US-0323460.  
PR 12-MAY-1995; 95US-0440421.  
PR 06-JUN-1995; 95US-0472934.  
XX  
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.  
XX  
PI Johnson GL;  
XX  
DR WPI; 2002-163179/21.  
DR P-PSDB; AAM48935.  
XX  
PT New isolated nucleic acid encoding mitogen extracellular  
PT signal-regulated kinase kinase, useful for gene therapy of e.g. cancer  
PT and for recombinant protein production  
XX  
PS Claim 2; Column 111-122; 125bp; English.  
XX  
CC The present invention provides the protein and coding sequences of a  
CC number of murine mitogen extracellular signal-regulated kinase (ERK)  
CC kinase kinase (MEK) enzymes. The sequences can be used to treat a wide  
CC range of diseases including cancer, autoimmune diseases, inflammation,  
CC allergies, degenerative neurological diseases and hormone-related  
CC diseases, and for inhibiting spermatogenesis or oocyte maturation for  
CC contraception. The present sequence is the murine MEK1.2 coding  
CC sequence.  
XX  
SQ Sequence 5539 BP; 1320 A; 1559 C; 1515 G; 1145 T; 0 other;  
Query Match 64.6%; Score 3387.6; DB 24; Length 5539;  
Best Local Similarity 83.4%; Pred. No. 0;  
Matches 4075; Conservative 0; Mismatches 709; Indels 102; Gaps 16;  
Qy 1 GAGAAATGGCGGGCGGGGGAATGGCGCTCTGCTCGGAGATTCGCGGGCCAGG 60

```

Db 298 GAGAAATATGGCGCGCGCGCGCGCATCGCGCTCGTCCGTGCGGATTCCTCCGCGCGCGCG 357
Oy 61 GTATACAGCCCTGAGGACGCGCGCGC-----GAGAGAGCCCTCAAGGCGACAC 111
Db 358 GCGGCGAGTCCCGAGGCGGCGCGCGCGGAGGAGGAGAGCTCTCAGGAGAACGCGG 417
Oy 112 GGGCCCGCGCGTGC-----GGAGTGTGTGCGGAGGCGGCGGAGCGGCGCGGAGCGG 168
Db 418 GCGCGCGCGCGCGCGCGCGCGCGGTGTGCGGAGCGTGGAGCGCGCGCGC-CGAGCGC 476
Oy 169 GCGGACTGCGGCGCGCGCGAGCTGCGCAAGTGGCGGAGTGGAGTGGACAGTGCCT 228
Db 477 GCGGACTGCGGCGCGCGCGGAGCGTCCCGCAAGTGGCGGAGTGGAGTGGACAGTGCCT 536
Oy 229 GAGGAGCCGCTCTTCTTCCGCGCTTACCGCGCGCTCTCGACT--TCCCGCGCGG 286
Db 537 GAGGAGCCGCTCTTCTTCCGCGCGCGCGCGCTGCGCGCTGCGCATCTACTTCCGCGCGG 596
Oy 287 AGCCCGCGGACGAGGCGGAGTGGGACGCGCTTCCAGCTGTGGGCGGCGCGCGCGC 346
Db 597 AGCCCGCGGACGCGGTGAGAGCGAGTCCGCTTCCAGCGCGC-CGCGGAGACCGCCACCGC 655
Oy 347 AGGAGCCCGGAGCGCGCGCGCGCGCCACCTTACGAGTGGTGGCGGCGCGGACAGCG 406
Db 656 GCGGAGCGCGGAGTGGCGTGGCGTCCGCTCCGACTGTGCGAGCGTGGCGCGCGCGGACAGCG 715
Oy 407 GCGCGTCAAGTCCCGCAGCGCGCGAGCCCGGAGAGAGCGCGCGCGCGCGCGCGCT 466
Db 716 GCGCGCGGAGCGCGCGCGG-----GCGGAGCGCG 745
Oy 467 CTCCTGACAGCGCGCGCGCGCGTCTGAGATGGAATAAAGAACTCTCAAGGCTTGC 526
Db 746 CCTCTGACAGCGCGCGCGCGTCTGAGAGATGAGAAATCAAGAACTCTCAAGGCTTGC 805
Oy 527 ACAAGTGAATGATGCTCCAGAGAAAGAAATGATCAGGAGAACTGAAGGCAACTGTA 586
Db 806 ACAAGTGAATGATGCTCCAGAGAAAGAAATGATCAGGAGAACTGAAGGCAACTGTA 865
Oy 587 TCCGAGCGTGAAGCAGAGATGTTGGAAGAAATAGCGGAGCGCTGTGTGTAA 646
Db 866 TCCGCGCGTGAAGCAGAGATGTTGGAAGAAATAGCGGAGCGCGCTGTGTGTAA 925
Oy 647 AACCAATCCCAATTAAGAGATGATCTGAAATGAATACTTAGAGCTGAGTCCGAG 706
Db 926 AACCAATCCCAATTAAGAGATGATCTGAAATGAATACTTAGAGCTGAGTCCGAG 985
Oy 707 GAGAGGTCAGGCAAGTGGCGCTTCCAGCTTCCAAAGCGGACGAGTCCCTCTCTG 766
Db 986 GAGAGGTCAGGCAAGTGGCGCTTCCAGCTTCCAAAGCGGACGAGTCCCTCTCTG 1045
Oy 767 GCAACTCCCAATCAGGTGCGCACATGGAATCTTCCAGAGTGAAGAGAAAAAG 826
Db 1046 GCAAGTCTTCCGAGGCGCTGCTGGAAGCCGGAATCCCAAGAGTGAAGAGAAAAAG 1105
Oy 827 TTTCCCGAGTGTCTTTTCAAGTGGCAGATCACACACCGCGGAGAGCGCTTACAG 886
Db 1106 TTTCCCGAGTGTCTTTTCAAGTGGCAGATCACACACCGCGGAGAGCGCTTACAG 1165
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Db 1166 ATGGCTTCCCGCGTACAGCCAGATAGAGACCAACTCTTCTGATGAGAGAGACAGTC 1285
Oy 947 CCAGACTGTACTTACTGACAGCAGATAGGCGCTAACCTTTTCTGATTTGAGAGAGACGC 1006
Db 1226 CCAGACTGTACTTACTGACAGCAGATAGAGACCAACTCTTCTGATGAGAGAGACAGTC 1285
Oy 1007 CAGAAATAATAATACGGGCTTATTTGGGCTCAGAACTGACAGCTGTGAGACAT 1066
Db 1286 CAGAAATAATAATACGGGCTTATTTGGGCTCAGAACTGACAGCTGTGAGACAT 1345
Oy 1067 TCTGTATTCATCTGCTATTTGTATGCTCCGGGTCTTCACTAGAACCTTAGACCCAA 1126
|||||
Db 1346 TCTGTATTCACCTCTTGTCTTGTATGCTCCGGTGTTTAGCTAGAACCTCTGACCCCA 1405
Oy 1127 TGTATGAGAAAAAACTTTAAAGAAATTTTGTAGGTGAGATTTGTTCCAGAAATATACA 1186
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Oy 1187 GTAGGCTGAGTCAAGGATCAAAAGCTCCATCTGTAAACCATCCGAAAGTTTGTTCAC 1246
Db 1466 GTAGGCTGAGTCAAGGATCAAAAGCTCCATCCGGAACCATCCGAAAGTTTGTTCAC 1525
Oy 1247 GCATGTCAAAATCTCATATCTTATCTATCTAGTACTTCTAGCTTACTAGAGAAAAA 1306
Db 1526 GCATGTCAAAATCTCATACACGTCTATCTGTAGCAATCCATCTACTTATAGAAAAA 1585
Oy 1307 GCATTAAGAGTGAAGAGGAGCAGATGTGCTATTTGCTTGTGGGCAATGCTTGAAG 1366
Db 1586 GCATTAAGAGTGAAGAGGAGCAGATGTGCTATCTGTGCTGGGCAATGCTTGAAG 1645
Oy 1367 AAGTCTTACATGTGTGAAAGCGGTGAGAGAACAGCTTGAATGCTCCCTTGTAGATCA 1426
Db 1646 AAGTCTTACATGTGTGAAAGCGGTGAGAGAACAGCTTGAATGCTCCCTTGTAGATCA 1705
Oy 1427 TTTGGCAGAGAGTGTAGAAAGAAATAGAGAACTTTAATATGTCCTTGTAGATCA 1486
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Db 1766 AGTGAATCTCATGATTTCTACAGCAGAGTGTGCAAGTCTGTGATTCCTCTTCT 1825
Oy 1547 CCTCAGAGCTGCACAGCAGCAACCGTACACAGAGCTTTGGTGTGATCA---CGAA 1603
Db 1826 CCTCAGAGCTGCACAGCAGCAACCGTACACAGAGCTTTGGTGTGATCA---CGAA 1885
Oy 1604 GGAATCAAGAGCAATTTTAACTTACTTATGAACTAGCAAACTCCGCTGCTT 1663
Db 1886 GGAATCAAGAGCAATTTTAACTTACTTATGAACTAGCAAACTCCGCTGCTT 1945
Oy 1664 ACAAGATTTTACCTGAGCCATGATTCAGTGTGGAATGGAATCTGTGCTGCTTAT 1723
Db 1946 ACAAGATTTTACCTGAGCCATGATTCAGTGTGGAATGGAATCTGTGCTGCTTAT 2005
Oy 1724 TTTCTAGAACTGGAATGTGAGAGATGCGCTCAGGCTTTCCTTCCATGATGACAG 1783
Db 2006 TTTCTAGAACTGGAATGTGAGAGATGCGCTCAGGCTTTCCTTCCATGATGACAG 2065
Oy 1784 GGGCCCTGCTTGGCAATTTGGGAGAGCAGTGAATTTCTGGGGCAGCAGTGAAGA 1843
Db 2066 GGGCCCTGCTTGGCAATTTGGGAGAGCAGTGAATTTCTGGGGCAGCAGTGAAGA 2125
Oy 1844 GCCCGAGTGGGAGAGCCACAGTGGCTTCCAGACAGATCTCAGAGATGTGTGG 1903
Db 2126 GCTTAAAGCCGCGGAGCGCAGCGGGTCTCCAGCCAGCATCTCAGAGGATGTGTGG 2185
Oy 1904 AGGCAATGTGAGCGCTTCTGTCAATGTGTGTGACCTCTCTCAAAAGTGTACGTTG 1963
Db 2186 AGGCAATGTGAGCGCTTCTGTCAATGTGTGTGACCTCTCTCAAAAGTGTACGTTG 2245
Oy 1964 CTGCTTTAAAAAATTTGAGAGCATGCTGTATTAATCTCTTGGCAGATTTAGGGAAA 2023
Db 2246 CTGCTTTAAAAAATTTGAGAGCATGCTGTATTAATCTCTTGGCAGATTTAGGGAAA 2305
Oy 2024 GAATCAAACTTCAAGACTTCTCAGCCAGCTTGTAGACACATCTTCAATGTGACAG 2083
Db 2306 GAATCAAACTTCAAGACTTCTCAGCCAGCTTGTAGACACATCTTCAATGTGACAG 2365
Oy 2084 ATGCCAATAGCCGCAAGTCAAGTGTCTCATATCAACACTGTTGGAACGTGCAAGGCC 2143
Db 2366 ATGCCAAGCCGCAAGTCAAGTGTCTCATATCAACACTGTTGGAACGTGCAAGGCC 2425
Oy 2144 AAGCAGAGAGTGTGAGAGTGTGAGAGAAATCTAAAAGCTGATTCATGTATGGTG 2203
Db 2426 AAGCAGAGAGTGTGAGAGTGTGAGAGAAATCTAAAAGCTGATTCATGTATGGTG 2485
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QY 2204 GTGTTAATATGCTTAATATGATTTCTGGAAACCAACTGAAATCAAAATTTGGCAG 2263  
DB 2486 GTGTCAATTACGCTTAAGTTGATCTTTGGAAACCAAGCTGAATCAAACTGCGCAG 2545  
QY 2264 AACTTCTGGCCGCTTGTCTATATAGTAAGTATGTTGTGGAAATTTCCGCTGAATTT 2323  
DB 2546 AACTGCTGGGCTGCTGCTTATATAGACAGGTGTGCTGGAAATTTCCGCTGAATTT 2605  
QY 2324 ATCCATATATGTCAGTACTGATGTTTCAACAGCTGAGCTGTTGAAATCAGTATAGA 2383  
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QY 2504 TGTTTTCAAAACCTGTTAAGAAATGCTGAGTGTTCAGTTCCACTCACTTCCAGAGATG 2563  
DB 2786 TGTTTTCAAGCTGTTAAGCAATGCTTAATGCTTCTGCTCCAGCTTCCAGAGATG 2845  
QY 2564 GTCCGCTTTGATGCTTATGTCAGATGAGGTGAATTTGCCGAAGCCATCAGTTGGCG 2623  
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QY 2624 TAAAGACACTTTGATGTCACAGACAGCTTCTTGACGAGTCTGTTCCCAACACT 2683  
DB 2906 TGAAGACACTGTCGATGAGGATCAGACAGCTTCTTGACGAGTCTGTTCCCAACACT 2962  
QY 2684 ATCTGAAACACAGACAGTTCCTCCGAGTGCACAGTCCACTTTAGAGAAACTGGA 2743  
DB 2963 GTCT-----AGAAACAGCTCCCTTGAAGACACAGTCCACTTTAGAGAAACTGGA 3013  
QY 2744 AAGGATTAATGCTTACAAATTAATGTCAGTTCAGAGACATTTCTGAGACCTGGCA 2803  
DB 3014 AAGGATTAATGCTTACAAATTAATGTCAGTTCAGAGACATTTCTGAGACCTGGCG 3073  
QY 2804 GCATTCAGTACGCTCTGATGTTCAACAAACAAACAAACAAACAAACAAACAAACAA 2863  
DB 3074 GCGTCTGTGAGACCTTCCAGCT-----CAACAAACAAACAAACAAACAA 3118  
QY 2864 AGCCAATGTTTCAAAACAAAGCAGACCCACAGTCACTGTTGAATCTCTCTCTTAT 2923  
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QY 2984 TACCAGCTGGCACTGCAGATGATGCTCTAAGATAGTACACTTCAAGGATTTATTCCTGCA 3043  
DB 3236 TCC-----CAGATATTTTAAAGCAGACCCAGGCAATTTGTTTCCCTGCA 3280  
QY 3044 GAATACCTTCTGATCTCTCAAAACAGGCAAGTTTCTCTACAAATTTCCAGAAACT 3103  
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QY 3104 GTCTCTCAAAACAGCTCAGATTAATTTCCAGCTTCTTCTTCTTCTTCTTCTTCTTCTG 3163  
DB 3341 GCTCTCAACACGAGACTCAGACAGCTCTCCAGCTTCTTCTTCTTCTTCTTCTTCTTCTG 3400  
QY 3164 CTTCCAGTATACATACAGGCAAGGCAAGCTTACAGTACCTACCCAGATTAATTAAGTAAAC 3223  
DB 3401 CTTCCAGTATACATACAGGCAAGGCAAGCTTACAGTACCTACCCAGATTAATTAAGTAAAC 3460  
QY 3224 AGGAGATCTCTCAAAACAGTACATGATCTGATGATGATGATGATGATGATGATGATGATG 3283  
DB 3461 TAGGAGACGCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3520  
QY 3284 ACACTTTGGCTGTAGCAGCAATAGTATGATGCTGTTATACCAAGTACGAGACAGTGT 3343  
DB 3521 ACAGCTTTGGCGCGCGCGGAGAGTGGCAACCCCGCATACCCAGGAGAGACAGTGT 3580  
QY 3344 TCAACCCAGTACAGGAGAAATGAGATTAATGATCAATACAGAGCTCAACTCCAGTATG 3403  
DB 3581 TCAACCCAGTACAGGAGAAATGAGATTAATGATCAATACAGAGCTCAACTCCAGTATG 3540  
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DB 3701 TCCCGCTCTCTCTGAAAGGCTGAAATGATGATGATGATGATGATGATGATGATGATG 3760  
QY 3524 ATTAATCAAGTCAAAAGATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3583  
DB 3761 ATTAATCAAAAGTCAAAAGATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3820  
QY 3584 TGGCAATGTCAGGCTCTCAGATGCTCCCTCCATAGTCTCTCAGCTGCAAGTGAAGTGA 3643  
DB 3821 TGGGAGATGTCAGGCTCTCAGATGCTCCCTCCATAGTCTCTCAGCTGCAAGTGAAGTGA 3880  
QY 3644 GAGAATATATCATATTATTCACAGATACACAGAGTCTTACAGAGATACCAAG 3703  
DB 3881 GAGAATATATATCATATTATTCACAGATACACAGAGTCTTACAGAGATACCAAG 3940  
QY 3704 CAATAACAGCTTATAGAAAGACATCAATGCTGAAAGTCAACAGATAGGCTTGGAG 3763  
DB 3941 CGAAACAGCTTATAGAAAGACATCAATGCTGAAAGTCAACAGATAGGCTTGGAG 4000  
QY 3764 CATTTCTCTCTTATACAGGCTCAAGATGTTGGAATCTGGAATCTTATGCTTAAAC 3823  
DB 4001 CATTTCTCTCTTATACAGGCTCAAGATGTTGGAATCTGGAATCTTATGCTTAAAC 4060  
QY 3824 AGTGACTTATGTCAGAAACATCTTCTGAGCAAGAAAGATGATGAAAGTCAAG 3883  
DB 4061 AGTGACTTATGTCAGAAACATCTTCTGAGCAAGAAAGATGATGAAAGTCAAG 4120  
QY 3884 AAGGATTAAGATGATGAGCATCTGATGATCAATCAATCAATCAATCAATCAATCAATCA 3943  
DB 4121 AAGGATTAAGATGATGAGCATCTGATGATCAATCAATCAATCAATCAATCAATCAATCA 4180  
QY 3944 CGTGTGAGAGACCAATTAATCTCTTCAATGATGATGATGATGATGATGATGATGATGATG 4003  
DB 4181 CGTGTGAGAGACCAATTAATCTCTTCAATGATGATGATGATGATGATGATGATGATGATG 4240  
QY 4004 ATTTGCTAGTAAATATGAGCTTCAAGAAATCAGTATTAATTAATTAATTAATTAATTA 4063  
DB 4241 ACCCTTGAATTAATATGAGCTTCAAGAAATCAGTATTAATTAATTAATTAATTAATTA 4300  
QY 4064 TACCTGCTGAGCTTCTGATCTCCATGAAACCAATCAATCAATCAATCAATCAATCAATCA 4123  
DB 4301 TACCTGCTGAGCTTCTGATCTCCATGAAACCAATCAATCAATCAATCAATCAATCAATCA 4360  
QY 4124 CCAATTTGCTAATTTGACAGCACTGTCAGAGACTTAAGATTTGAGATTTGAGACTGAG 4183  
DB 4361 CCAACCTGCTCATTTGACAGCACTGTCAGAGACTTAAGATTTGAGATTTGAGACTGAG 4420  
QY 4184 CCAAGTTGCAATCAAAAGAACTGTCAGAGAGATTTCAAGGCAATTAATTAATTAATTA 4243  
DB 4421 CCAAGTTGCAATCAAAAGAACTGTCAGAGAGATTTCAAGGCAATTAATTAATTAATTA 4480  
QY 4244 TTGATTTATGAGCACTGAGTACTAGAGTCAACGATTAAGAAAGAGTCTGATGATGAT 4303  
DB 4481 TTGATTTATGAGCACTGAGTACTAGAGTCAACGATTAAGAAAGAGTCTGATGATGATGAT 4540  
QY 4304 GGAATGTTGGCTGTCTATTAAGAAATGCTTGTGCAAAACCACTGGAATGACAGAA 4363  
DB 4541 GGAATGTTGGCTGTCTATTAAGAAATGCTTGTGCAAAACCACTGGAATGACAGAA 4600  
QY 4364 AACCTCAATCAATCTTGTGATTAATTAAGATGCTAGTCAACTGCTCATGCA 4423



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Db 4601 AACACTCCACATATCTCGCTTGATATTTAGATTGTCAGCCAACTACTGACCGTCCA 4660
Oy 4424 TCCCTTTCACATTTGTCCTCGTTTACGAGATGTGGCTCTCTGTTTGAACCTTCAAC 4483
Db 4661 TCCCGTCAACACTGTCGCCGGGTGCGGAGAGTGGCGCTGGCTTGAACCTTCAAC 4720
Oy 4484 CTCAGACAGACCTCCATCAGAGAGCTAGTAAGATCCAGTCTTTGCTACTACTGT 4543
Db 4721 CTCAGACAGCGGCTCCGTCACAGAGAGCTGTAACATCCGCTTCCCTACCAGCTGT 4780
Oy 4544 AGCCATTATGACATCACTACAGTAGAAGAGATGCTCAAGAAAGAAAAAACTT 4603
Db 4781 AGTTAAATTTAGATACCTCTTAATGGAGACAGATATGCAACGGGAGAGAAAGA 4840
Oy 4604 G----TGGGGGAACACATTGATATTTCTACTGCGCATGTATGCCATGACAGCTATGAAG 4659
Db 4841 GAACTTGGGGGAGACATGCGCTTAACCGCACCCCTCAACGCCATGAAACAGCAAGAAAG 4900
Oy 4660 AGCCAGTGGGGAACCCCTTACTAGTATGTATGATGACAAATCATGATCTTACTAAC 4719
Db 4901 GGGCCAGCGGGGAA--CCGTACTTAAGCATGTGATTGACAAATCATGACCTGTACTAAC 4959
Oy 4720 TCAGTATGCA--AAAGCCCAAACTAGTGCAGAAAGTAACTGCTTCAAGAAAGT 4778
Db 4960 TCGATATGACAGATCTACAGCTGCTGACAGACTGACACCGCTTTCACAGAGACTG 5019
Oy 4779 GCCCTAGGTGAACAGAGAAACAATGAAGTTTGCATGACTAAATTCACAGAGCATATTT 4838
Db 5020 GCTGTGGGGAGACAGAGAGGCGATGAGTTTGCATGACTAAAGAAACAGAGCATATTT 5079
Oy 4839 ATTTTGTGGAGCACTTTTTCAGCAA 4864
Db 5080 A--TTTTTGAGCACTTTTTCAGCTA 5103

RESULT 8
AA225069
ID AA225069 standard; cDNA: 3911 BP.
Oy AA225069;
AC AA225069;
DT 09-DEC-1999 (first entry)
DE Human MEK1 nucleotide sequence.
Oy MEK1; MEK2; MEK3; mitogen-activated protein kinase; MAPK; ERK;
KW extracellular regulated kinase; signal transduction; regulation;
KW MAPK/ERK; MEK; MKK; inflammation; cellular proliferation;
KW differentiation; development; cell death; ss.
Oy Homo sapiens.
OS Homo sapiens.
FH Key 3.3911 Location/Qualifiers
FT CDS /*tag- a
FT /product= "MEK1"
FT
Oy WO9947686-A2.
Oy 23-SEP-1999.
Oy 15-MAR-1999; 99WO-US055556.
Oy 16-MAR-1998; 98US-0078153.
Oy 04-SEP-1998; 98US-0099165.
Oy (CADU-) CADUS PHARM CORP.
Oy Johnson GL;
Oy WPI; 1999-571843/48.
Oy P-PSDB; MAY42104.
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XX New human MEK1 polynucleotides and polypeptides, used for regulating
PT signal transduction in cells -
PS Claim 2; Fig 1; 159pp; English.
XX
CC The present sequence encodes human mitogen-activated protein kinase/
CC extracellular response kinase (MAPK/ERK) kinase kinase (MEK),
CC specifically designated MEK1. The MEK proteins are used to modulate
CC and regulate signal transduction in cells, as well as for regulation of
CC gene transcription in a cell encoding MEK, where the cell is involved
CC in inflammation, regulation of cellular proliferation and
CC differentiation, regulation of development, regulation of cell death or
CC regulation of inflammation. They are also used to prepare antibodies.
CC MEK polynucleotides can be used to produce the protein recombinantly
CC and as a source of probes and primers.
SQ
Sequence 3911 BP; 1058 A; 973 C; 975 G; 905 T; 0 other;

Query Match 62.7%; Score 3286.4; DB 20; Length 3911;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 3580; Conservative 0; Mismatches 331; Indels 45; Gaps 5;

Oy 590 CAGCCTGGAGACAGAAATGTTGGAAGAGAAATAGCGAGGCTGTGCTGTAAGC 649
Db 1 CGGCTGGAGAGACAGATGGTTGGAAGAGAAATAGCGAGGCTGTGCTGTAAGC 60
Oy 650 CAATCCAGATTAAAGAGATGATCTGAATGAATCACTTACAGCTGAGTCCAGAG 709
Db 61 CAATCCAGATTAAAGAGATGATCTGAATGAATCACTTACAGCTGAGTCCAGAG 120
Oy 710 AGGTCCAGGCAAGTGGCGCTTCCAGAGTCCAAAGGCCGAGCGAGTCTCTGCA 769
Db 121 AGGTCCAGGCAAGTGGCGCTTCCAGAGTCCAAAGGCCGAGCGAGTCTCTGCA 180
Oy 770 ACTCCCAATCAGTGGCGAGTGAATGAAATCAATCTCCAGAGTAAAGAAAGTTT 829
Db 181 ACTCCCAATCAGTGGCGAGTGAATGAAATCAATCTCCAGAGTAAAGAAAGTTT 240
Oy 830 CCCAGTGGCTTTTCAAGTGGAGAAATCACACACCCCGAGAGAGCCCTTCCAGAG 889
Db 241 CCCAGTGGCTTTTCAAGTGGAGAAATCACACACCCCGAGAGAGCCCTTCCAGAG 300
Oy 890 GCTTCTACACATATAGCCCTGAGAAACACCGCGTGTTAACAAAGTATGCGGCCA 949
Db 301 GCTTCTACACATATAGCCCTGAGAAACACCGCGTGTTAACAAAGTATGCGGCCA 360
Oy 950 GACTGTACTTACTGAGAGATAGGCGCTAATCTTCTGATTTGGAGAGACCCAG 1009
Db 361 GACTGTACTTACTGAGAGATAGGCGCTAATCTTCTGATTTGGAGAGACCCAG 420
Oy 1010 ACAATTAATACCGGCTGTTTATTTGGCTCAGAACTGACAGTGCAGTGAACATCT 1069
Db 421 ACAATTAATACCGGCTGTTTATTTGGCTCAGAACTGACAGTGCAGTGAACATCT 480
Oy 1070 GATTCATCTGCTATTTGTGATGCTCGGGGTGTTCAACTAGAACCTTCAAGCCATGT 1129
Db 481 GATTCATCTGCTATTTGTGATGCTCGGGGTGTTCAACTAGAACCTTCAAGCCATGT 540
Oy 1130 TATGAGAAAACTTAAAGAAATTTAGTGTGAGATTTGTTCCAGAAATATCAGATA 1189
Db 541 TATGAGAAAACTTAAAGAAATTTAGTGTGAGATTTGTTCCAGAAATATCAGATA 600
Oy 1190 GCGTAGCTCAAGATCAAGAGCTCATCTCGTAACACCATCCAGAAAGTTTGTACGCA 1249
Db 601 GCGTAGCTCAAGATCAAGAGCTCATCTCGTAACACCATCCAGAAAGTTTGTACGCA 660
Oy 1250 TGTCAATTTCTATCATTTGTCATCATCTAGTACTTCTAGCTTGTAGAAAACAGCA 1309
Db 661 TGTCAATTTCTATCATTTGTCATCATCTAGTACTTCTAGTACTTGTAGAAAACAGCA 720
Oy 1310 TAAAGGATGAAGAGAACAGATGTCTCTATTTGTTGGGATGCTGTATGAAGAA 1369
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Db 721 TAAAGATGAAGAGACAGATGTGTCTATTGCTTGTGGGCAATGCTGATGAAGAA 780  
Oy 1370 GTCTTACAGTGTGTGAAGAGCGCTGCAGAGAACAGCTGCACCACTGCATGTCAATTT 1429  
Db 781 GCTTACAGTGTGTGAAGAGCGCTGCAGAGAACAGCTGCACCACTGCATGTCAATTT 840  
Oy 1430 GGGCAGAGAGTGTAGAGAAATAGAGAACTTTATATGTCCCTTTTGTAGTCTAACT 1489  
Db 841 GGGCAGAGAGTGTAGAGAAATAGAGAACTTTATATGTCCCTTTTGTAGTCTAACT 900  
Oy 1490 GAGAGCTCATGATTTCTACAGCAGAGATTTGCAAGCTCTGTGATGCCCTTCTTCCC 1549  
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Oy 1550 TCAGAGCTGCACAGCAGCAAACTGACAGCAGAGCTTGGCTGATCAGCAAGAAATC 1609  
Db 961 TCAGAGCTGCACAGCAGCAAACTGACAGCAGAGCTTGGCTGATCAGCAAGAAATC 1020  
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Oy 1670 ATTAGCTGAGCCATGATTTAGAGTGTGAAATGGAACCTGTTGCTTATTTCTA 1729  
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Oy 1730 GAAACTGGAATGTGAGAGATGCCCCAGCGCTTTCCATGATGTCAATGGGGCCC 1789  
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Oy 1790 TGTCTGTGGCAAAATGGGGAGACACTGGAATTTCTGGGGGAGAGTGGAAAGAGCCCA 1849  
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Db 1261 GGGGGAGAGCGGCGAGCGGCTCTCCACAGCAGATCTCAGAGATGTGGTGGAGCGCT 1320  
Oy 1910 GCTGACGCTCTGTCAATGGTGTGTGTGACCCCTGTCAAAAGTGTACGTGTCTT 1969  
Db 1321 GCTGACGCTCTGTCAATGGTGTGTGTGACCCCTGTCAAAAGTGTACGTGTCTT 1380  
Oy 1970 TAAAAACATTTGAGAGCCTATGCTATATACCTCTTCCACAGATTAGGGGAAAGATCA 2029  
Db 1381 TAAAAACATTTGAGAGCCTATGCTATATACCTCTTCCACAGATTAGGGGAAAGATCA 1440  
Oy 2030 AACTTCAGAGACTCTCCAGCAGTGTGTGACACACATCTCAATGTCAGATGCCA 2089  
Db 1441 AACTTCAGAGACTCTCCAGCAGTGTGTGACACACATCTCTTCAAGTGTGAGATGCCA 1500  
Oy 2090 ATAGCCGACAAAGTACGTGTCCATATCAACACTGTTGGAACCTGTCAAAAGGCCAAG 2149  
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Oy 2390 TGTGCTCTTAACTTGTGCTTGCATTTGATTAATTTCCACTGAATGTGGCAAG 2449  
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Oy 2450 TTTCCAGAAAGATCTACTTGAAGTCTGCAAGATGGTTACTACAGTACCCATGTGTTT 2509  
Db 1861 TCTCTCGAGAGATATCTAGACTCTGCAGAGATGGTGCACCCAGTCCCGCTGTGTTT 1920  
Oy 2510 CAAACTGTAGAAATGCTGAGTGTTCAGTTCACCTACTCTACCTACAGATGCGTCCG 2569  
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Oy 2570 GTTGTATGCTATATGAGATGAGGTGAATGGCAATGCCAATCCAGTTGGGCGTGAAG 2629  
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Oy 2690 AAACAGAGAAAGCTTCCCTGAGTGCAGAGTCCATTTAGAGAAATCTGAAAAAGAT 2749  
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Db 2149 TATGTCTACAAAATTTAGTGCAGTTCAGAGACATTTCTGAGAGCTGGCCAGCTCT 2208  
Oy 2810 CAGTAGGACCTTCTAGTTCACACAAACAAACAAACAGAGCAACCAAGCCAA 2869  
Db 2209 CAGTAGGACCTTCCACACT-----CAACAAACAGAGCAACCAAGCCAA 2253  
Oy 2870 TGTGTTAAACAAAAGCAGACCCACAGTCAAGTGTGAACTCTCTTATCTCATC 2929  
Db 2254 CGGTTAAACAAAAGCAGACCCACAGTCAAGTGTGAACTCTCTCTCTCTCTCTCTCT 2310  
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Db 2311 ATGCTCAATTAATGTTTCCAGCTTGTCAACCCCTTCTCTTACCCCATCTGTACAG 2367  
Oy 2990 CTGGCACTGCACAGATGTCTTAACATAGACTTCAGGAGATTCATTTCCCTGCAGATAC 3049  
Db 2368 -----CAGATTTTCTTAACACAGACCCAGGACTTTGTTCCCTGCAAAAATAC 2415  
Oy 3050 CTCTGCTATCTCTCTCAAAACAGAGCAGATTTCTCTACAAATTCACAGAACTGTCTG 3109  
Db 2416 CTCTGCTATCTCTCTCAAAACAGAGCAGATTTCTCTCTTAATTTCCAGAGAACTGTCTG 2475  
Oy 3110 AAAACAAAGACTCAGATTAATCTTCCAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCA 3169  
Db 2476 AACACGAGACTCAGAGCTCA 2535  
Oy 3170 GTAACTACACAGGCCCAAGCCATCTAGACCTAACCCAGGTAATACAGTAACAGAGAG 3229  
Db 2536 GTAACTACACAGGCCCAAGCCATCTAGACCTAACCCAGGTAATACAGTAACAGAGAG 2595  
Oy 3230 ATCCCTCAAAAAATACATGACACTGTGATCTGAACAGTGTGTTCAATGTGATGACGT 3289  
Db 2596 ACGCCCAAAAAATACATGACACTGTGATCTGTGGCAGTCTTCCAGAGTGTGAGACAGCT 2655  
Oy 3290 TTGGCTGTGACAGCATATGATATGATGTGTATGATGATGATGATGATGATGATGATGAT 3349  
Db 2656 TTGGCTGTGACAGCATATGATATGATGTGTATGATGATGATGATGATGATGATGATGAT 2715  
Oy 3350 CAGTAGAGAGAAATCAGATATGATGTCAATACAGAGCTCAACTCAGATATGAGAGAC 3409  
Db 2716 CAGTAGAGAGAAATCAGATATGATGTGATGTGATGATGATGATGATGATGATGATGAT 2775  
Oy 3410 TTTCTTAAGCATATATGCTCTCAAGTGTATCAACAGTAACTTTAAGTCAAGAGTGTCTG 3469  
Db 2776 TTTCTTAAGCATATATGCTCTCAAGTGTATCAACAGTAACTTTAAGTCAAGAGTGTCTG 2835  
Oy 3470 TCTGCTCTCTGAAAGGCTGAAAGATGATGATCTCAACAAAGATGATGATGATGATGATGAT 3529  
Db 2836 TCTGCTCTCTGAAAGGCTGAAAGATGATGATCTCAACAAAGATGATGATGATGATGATGAT 2895

QY	3530	AAAAGTCAAAAGAGACATGAGCTGGAAGAAACAAACCTTTACCAATTTGGCATGGCAA	3589
Db	2896	AAAAGTCAAAAGAAAGATGGAAGCTGMAAGAGAGAGAGCTTTACGATCCGATGGCGCA	29555
QY	3590	TGTACGGCTCTCAGAGATGCCCTCCCAATAGTTCCTACGTCAGAGTTGAAATGGAGAAG	3649
Db	2956	TGTACGGCTCTCAGAGATGCCCTCCCAATAGTTCCTACGTCAGAGTTGAAATGGAGAAG	3015
QY	3650	ATATCATCATATTTAAACAGAGATACACAGAGACTCTTACAGAGCATATCCAAAGCAAAAC	3709
Db	3016	ATATTCATCATTCATTCAGCAGAGAACACACAGAAACTTCTCAGAGCATATCCAAAGCAAAAC	3075
QY	3710	AACCGTATAGAGAAACACTGAAATGGCTGAAAGTCAACAGATAGGCGCTTGAGACATTTT	3769
Db	3076	AGCCTTACAGAGAAAGACGCTGAGTGGCTGAAAGGCGCAGACAGATAGGCGCTTGAGACATTTT	3135
QY	3770	CTTCTGTATTACAGGCGTCAAGATGTGGGAACTGGAACTTATAGGCTGTAAACAGGTGA	3829
Db	3136	CTTCTGTATTACAGGCGTCAAGATGTGGGAACTGGAACTTATAGGCTGTAAACAGGTGA	3195
QY	3830	CTTATGTACAGAAACACATCTTCTTGAGCACAGAGAAAGTAGTAGAACACTTAGAGAGAGA	3889
Db	3196	CTTATGTACAGAAACACATCTTCTTGAGCACAGAGAAAGTAGTAGAACACTTAGAGAGAGA	3255
QY	3890	TAAACATGATGAGCGCATCTGAATCATCCAAACATCATTTAGATATGTGGAGGACACGTGTG	3949
Db	3256	TAAACATGATGAGCGCATCTGAATCATCCAAACATCATTTAGATATGTGGAGGACACGTGTG	3315
QY	3950	AGAGAGCAATTCACATCTCTTCATTGAATGGATGGCAGAGGGGATCGGTGGCTCATTTGC	4009
Db	3316	AGAGAGCAATTCACATCTCTTCATTGAATGGATGGCAGAGGGGATCGGTGGCTCATTTGC	3375
QY	4010	TGATTAATATTTGGAGCGCTTCAAAAGATCAGTATGTTATTAACATACACTAACAGTTACCC	4069
Db	3376	TGATTAATATTTGGAGCGCTTCAAAAGATCAGTATGTTATTAACATACACTAACAGTTACCC	3435
QY	4070	GTTGGCTTTTCGTATCTCCATGAAAACCAATCATTTCCACAGAGATGTCAAGGTGGCAATT	4129
Db	3436	GTTGGCTTTTCGTATCTCCATGAAAACCAATCATTTCCACAGAGATGTCAAGGTGGCAATT	3495
QY	4130	TGCTAATATGACAGACATGGTCACAGACTAGAAATTCGATTTTGGAGCTGCAGCAGAGT	4189
Db	3496	TGCTAATATGACAGACATGGTCACAGACTAGAAATTCGATTTTGGAGCTGCAGCAGAGT	3555
QY	4190	TGGCATCAAAAGAACTGTGTGACGAGAGATTTTCAGGGACAATTTACTGGGGACAATTGCAT	4249
Db	3556	TGGCATCAAAAGAACTGTGTGACGAGAGATTTTCAGGGACAATTTACTGGGGACAATTGCAT	3615
QY	4250	TTATAGGACCTGAGAGTACTTAAGAGGTTCACACAGATTTGGAAAGAGCGTGTATGTAGAGATG	4309
Db	3616	TTATAGGACCTGAGAGTACTTAAGAGGTTCACACAGATTTGGAAAGAGCGTGTATGTAGAGATG	3675
QY	4310	TTGCGCTGTGTATTTAGAAATGGCTTGTGCAAAACCAACCATGGAATCAGAAAAAACT	4369
Db	3676	TTGCGCTGTGTATTTAGAAATGGCTTGTGCAAAACCAACCATGGAATCAGAAAAAACT	3735
QY	4370	CCATATCATCTTGCTTGATATTTAATATGCTATGTGCAACTACTCTCATCATCATCTT	4429
Db	3736	CCATATCATCTTGCTTGATATTTAATATGCTATGTGCAACTACTCTCATCATCATCTT	3795
QY	4430	CACATTTGTCTCCGTGTTACGAGATGTGGCTTCTGTTGTTTAAACCTTCAACCTCAGG	4489
Db	3796	CACATTTGTCTCCGTGTTACGAGATGTGGCTTCTGTTGTTTAAACCTTCAACCTCAGG	3855
QY	4490	ACGAGCTCCATACAGAGAGCTACTGAAACATCCAGTCTTTCGTACTCATGTGAG	4545
Db	3856	ACGAGCTCCGTACAGAGAGCTACTGAAACATCCAGTCTTTCGTACTCATGTGAG	3911

RESULT 9  
AAx80912  
ID AAx80912 standard; cDNA; 3911 BP  
xx

AC	AAx80912;
XX	
DT	03-NOV-1999 (first entry)
XX	
DE	Human MEK1 cDNA.
KW	Human MEK1 cDNA; Mitogen ERK kinase kinase 1 protein; MEK1; protease;
KW	extracellular signal regulated kinase; ERK; signal transduction pathway;
KW	regulation; apoptosis; protein kinase; cleavage; caspase; antibody;
KW	kinase fragment; mutant MEK1 protein; NH2-terminal fragment; detection;
KW	immunoreactive; diagnostic; therapeutic assay; reagent; disorder;
KW	aberrant expression; activation; MEK1 gene product; DNA probe; primer;
KX	selectively hybridise; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 3..3911
FT	/tag= a
FT	/product= "MEK1 protein"
FT	/function= "Regulates cellular apoptosis"
FT	mat_peptide 2052..3908
FT	/tag= b
FT	/note= "Active fragment that mediates apoptosis"
XX	
PN	M09941385-A1.
PD	19-AUG-1999.
XX	
PE	12-FEB-1999; 99WO-US02974.
XX	
PR	13-FEB-1998; 98US-0023130.
XX	
PA	(CADU-) CADUS PHARM CORP.
XX	
P1	Johnson GL;
DR	WPI; 1999-508649/42.
DR	P-PSDB; AAY26235.
XX	
P1	A new mammalian serine-threonine protein kinase for treating
PT	disorder characterized by aberration of the enzyme gene
XX	
PS	Claim 5a; Page 124-130; 149pp; English.
CC	The present sequence is an isolated human MEK1 cDNA. It encodes
CC	Mitogen ERK kinase kinase 1 (MEK1) protein, which functions to
CC	integrate proteases and signal transduction pathways involved in the
CC	regulation of apoptosis. It is a 196 kDa protein kinase, which upon
CC	cleavage at Asp 681/684 by caspase generates a 91 kDa kinase fragment
CC	that induces apoptosis and a 113 kDa NH2-terminal fragment. Mutant MEK1
CC	proteins that are resistant to cleavage by caspase proteases and capable
CC	of inhibiting apoptosis can be produced. MEK1 proteins and antibodies
CC	immunoreactive with MEK1 proteins are used in diagnostic and therapeutic
CC	assays and reagents for detecting and treating disorders involving
CC	aberrant expression or activation of the MEK1 gene products. DNA probes
CC	or primers that selectively hybridize to MEK1 cDNA, can be used for its
CC	detection in samples.
XX	
SQ	Sequence 3911 BP; 1058 A; 973 C; 975 G; 905 T; 0 other;
	Query Match 62.7%; Score 3286.4; DB 20; Length 3911;
	Best Local Similarity 90.5%; Pred. No. 0;
Db	Matches 3580; Conservative 0; Mismatches 331; Indels 45; Gaps 5
OY	550 CAGCCTGGAAGCAGCAATGGTTGGAAAGAGAATAATGCGGAGGCCCTGTGGTGTAAAC 649 1   Dd 1 CGGCCTGGAAGCACAGTGTTGGAAAGAGAATAATGCGGAGGCCCTGTGGTGTAAAC 60
OY	650 CAATCCAGATTAAAGAGATGAGTGTGAAATAATCATCACTTAGCAGTGAGTCCTCCAGAG 709 1   Db 61 CAATCCAGATTAAAGAGATGAGTGTGAAATAATCATCACTTAGCAGTGAGTCCTCCAGAG 120

QY	710	AGGTCCAGGCAATGTCGGGCTTCA	CACAGCTTCCAAGGGCGACGAGCTCTCTCGGCA	769
Db	121	AGGTTCACAGGCAAGTCGGCTTCA	CCAGCTTCCAAAGGGCGACGAGCTCTCTCGGCA	180
QY	770	ACTGCCATCAGGTCGCGACGTGA	AAATCTCCAGAGTAAGGAGAAAAAGTTT	829
Db	181	ACTCCCATCAGGTCGCGACGTGA	AAATCTCCAGAGTAAGGAGAAAAAGTTT	240
QY	830	CCCCAGTGCCTTTTCAGAGTGG	CAGATCCACACACCCCGAAGAGCCCTTTCACAGATG	889
Db	241	CCCCAGTGCCTTTTCAGAGTGG	CAGATCCACACACCCCGAAGAGCCCTTTCACAGATG	300
QY	880	GCTTCTCACCATATAGCCCTG	AGAAAACAACCCCGGTATTAA	CAAGATGATGCGGCGCA 949
Db	301	GCTTCTCACCATATAGCCCTG	AGAAAACAACCCCGGTATTAA	CAAGATGATGCGGCGCA 360
QY	950	GACGTACTTACCTCAGACAGAT	AGGCGTTACCTTCTGATTTGG	AGAGACACCCAG 1009
Db	361	GACGTACTTACCTCAGACAGAT	AGGCGTTACCTTCTGATTTGG	AGAGACACCCAG 420
QY	1010	ACAAATAAATACCGGGCTTTT	ATTGGGCGTCAGAACTGC	ACGCTGACGTGGAGATCTT 1066
Db	421	ACAAATAAATACCGGGCTTTT	ATTGGGCGTCAGAACTGC	ACGCTGACGTGGAGATCTT 480
QY	1070	GTAATCATCTGCTATTTGT	GTGATGCTCGGGGTGTTTCA	CTAGAACCTTCAGACCAATGT 1129
Db	481	GTAATCATCTGCTATTTGT	GTGATGCTCGGGGTGTTTCA	CTAGAACCTTCAGACCAATGT 540
QY	1130	TATGAGAAAAACCTTTAA	CAATTTTGTAGTTTGTTC	CCAGAAATATCACAGTA 1188
Db	541	TATGAGAAAAACCTTTAA	CAATTTTGTAGTTTGTTC	CCAGAAATATCACAGTA 600
QY	1190	GGCGAGCTCAAGATCAAA	GCCTCCATCTGTACACATCC	AGAAATTTGTTTTCAGCA 1249
Db	601	GGCGAGCTCAAGATCAAA	GCCTCCATCTGTACACATCC	AGAAATTTGTTTTCAGCA 660
QY	1250	TGTCAAAATTCATCATCT	GTCAATCTTCAAGTCTATG	TCTTACAGAAAACAGCA 1309
Db	661	TGTCAAAATTCATCATCT	GTCAATCTTCAAGTCTATG	TCTTACAGAAAACAGCA 720
QY	1310	TAAAGGATGAAGAGAAC	CAATGTGTCTATTGCTTTG	TGGGCATGCTTATGAAGAA 1366
Db	721	TAAAGGATGAAGAGAAC	CAATGTGTCTATTGCTTTG	TGGGCATGCTTATGAAGAA 780
QY	1370	GCTTTCACAGTGTGGA	GAGCGGCGGAGAAACA	AGTGTGACCAACATCTGATCAATTT 1429
Db	781	GCTTTCACAGTGTGGA	GAGCGGCGGAGAAACA	AGTGTGACCAACATCTGATCAATTT 840
QY	1430	GGGCGAAGAGTGTAGA	AAATAGAAACCTTTAAT	TATGTCCTTGTATAGTTAAT 1489
Db	841	GGGCGAAGAGTGTAGA	AAATAGAAACCTTTAAT	TATGTCCTTGTATAGTTAAT 900
QY	1480	GGAATCTCATGATTTT	TACAGCCAGAGTGTCA	AAAGTCTCTGATTTCCCTTTTCC 1549
Db	901	GGAATCTCATGATTTT	TACAGCCAGAGTGTCA	AAAGTCTCTGATTTCCCTTTTCC 960
QY	1550	TCAGAGCTGCACAG	CACAAACCGTACAG	CAGACGACCTTTGGGTGATACGAAGAAATC 1609
Db	961	TCAGAGCTGCACAG	CACAAACCGTACAG	CAGACGACCTTTGGGTGATACGAAGAAATC 1020
QY	1610	AAGAGAGCAATTTAA	CCCTTACTATATGAA	CTCAGCAAAATCCCTCTGTTTCAAG 1666
Db	1021	AAGAGAGCAATTTAA	CCCTTACTATATGAA	CTCAGCAAAATCCCTCTGTTTCAAG 1080
QY	1670	ATTTAGCTGAGCCAT	TGATTCAGGTGTTTGG	AATGGAATCGTTGGCTGCTTATTTCTTA 1729
Db	1081	ATTTAGCTGAGCCAT	TGATTCAGGTGTTTGG	AATGGAATCGTTGGCTGCTTATTTCTTA 1140
QY	1730	GAAACTGGAATGTAG	AGATATGGCCCTGAG	CGCTTTCCATGATGTCATGCGGGGCC 1789
Db	1141	GAAACTGGAATGTAG	AGATATGGCCCTTAT	AGCGCTTTTTCACACGCACTGTAATGTGGGGCC 1200
QY	1790	TGCTGTGTGGCAAT	GGGAGAGCACTG	GAATTTCTTGGGGCGACAGTGTAAACCCCGA 1849

Db	1201	TTTTTTTTTTGGCAAAAGGGGAGNGCACTGGAAACTCTGGAGGCGGCACTGGGGCACACTTAA	1260
Qy	1850	GTGGGGGAGGCCAACAGTGGGGGCTTCCGACACAGTATATCTAGAGATGTGGTGGAGCGAT	1909
Db	1261	GGCGGGGAGCGGCCAGGGGGGCTCCGACGCCAGCAATCTGAGGGGATGTGGTGGAGGGGT	1320
Qy	1910	GCTGCAGGCTTCTGCTCAATGGTCTGTCTCAACCTGTCTACAAAGTGTACGTGGTGGCTT	1969
Db	1321	GCTGCAGTGTCTGTCTCAATAGTCTGGGCTTACCTGTCTACAAAGTGTACGTGGTGGCTT	1380
Qy	1970	TAAAAACATTAGAGCCATGCTGGTATATACTCTTGCACAGTTTATGGGAAAGATCA	2029
Db	1381	TAAAAACATTAGAGCCATGCTGGTATATACTCTTGCACAGTGTGCGAGAAAGATCA	1440
Qy	2030	AACCTCAGAGACTCTCCAGCCATGTTATACACACATCCCTAGTCAAAATGTGCAGATGCCA	2088
Db	1441	AACCTCAGAGACTCTCCGCGCAATGTTATACACTATCTGTCAAGTGTGCAGATGCCA	1500
Qy	2090	ATAGCCGCAAGTACAGTGCCTCCATATCAACACTGTTGGAACTGTCCAAAGGCCCAAGCAG	2149
Db	1501	ACAGCCGCAACAGTACAGTGCCTCCATATCTACAGTGTGGAATCTGTCCAAATGCCCAAGCAG	1560
Qy	2150	GAGAGTTGGCAGTTGGCAGAGAAATACTAAAGCTGGATTCATTGGTATGGTGGTGTG	2209
Db	1561	GAAAGCTGGCGGTTGGGAGAGAAATACTTAAAGCTGGGTCCATCGGGGTTGGTGGTGTG	1620
Qy	2210	ATTATGTCTTAAATTTGTAATTTCTTGGAAACCAAACTGATCAAACTTATGGCAGAACTTC	2269
Db	1621	ATTAGGTTTAAAGTTGTAATCTTGGAAACCAAACTGATCAAACTTATGGCAGAACTTC	1680
Qy	2270	TGGCGCGCTTGTCTTATAGATATGAGTATGAGTGTGGAAATTCCTGCTGAATTTATNCCTC	2329
Db	1681	TGGGTCGCTCTGTCTTATAGACAGGTTGCTGTGGAAATTCCTGCTGAATTTATNCCTC	1740
Qy	2330	ATATGTGAGTACTGATGTTTCCAAAGCTAGGCTGTGAAATCAGGTATTAAGAGCTGC	2389
Db	1741	ATATGTGAGTACTGATGTTTCCAAAGCTAGGCTGTGAAATCAGGTATTAAGAGCTGC	1800
Qy	2390	TGTCCTCTTAAACCTTTGCTTTGCGAGTCCATTAATTCACCTCATATGTGGCCAAAC	2449
Db	1801	TCTCCCTCTTAAACCTTTGCTTTGCGAACTCAATTAATTCACCTCATATGTGGCCAAAC	1860
Qy	2450	TTTCCAGAAAGATCTACTGTAGTGTCTGCAAGAAAGGTATCTACAGTACCCCATGTGTTT	2509
Db	1861	TCTCTCGAAGATATATCTGAGCTCTGCGCAGATGGTGAACCGCAGTGCCTGTGTGTTT	1920
Qy	2510	CAAAACCTTTAGAAATGCTGAGTGTTCAGCTTCCACTACTACTACACAGATGCGTCCG	2569
Db	1921	CCAAAGCTGTAAACATGCTTAAATGCTTCTGGTCTCCACCCACTTCAACAGATGCGCCGCG	1980
Qy	2570	GTTTATGTGCTATTGTCAGATGAGGTGGAATTTGCCCAAGCCATCCAGTTGGGCGTAGAG	2629
Db	1981	GTTTATGTGCTATTGTCAGATGAGGTGGAATTTGCCCAAGCTTCCAGTGGGCGTAGAG	2040
Qy	2630	ACACTTGGATGGTCAACAGGACAGCTTCTTGAGGCAATCTGTCCCAACACTATCTGG	2689
Db	2041	ACACTTGGATGGTCAATCAGACAGCTTCTTGAGGCAATCTGTCCCAACACTATCTGG	2095
Qy	2690	AAACCCAGAGAGAGTTCCTTCACTAGTGCACACTTCATTAGAGAAATCTGAGAAAGAT	2749
Db	2096	-----AGAAACAGAGCTCCCTTGAGCAGACACTTCATATAGAGAAATCTGAGAAAGATC	2148
Qy	2750	TATGTGCTACAAATTTGAGTGCAGTTTCAGAGACATTTCTGAGAGCTGGCCAGCATTTT	2809
Db	2149	TAAAGTGTACAGAGCTAGTGGCCAGCTCGGAGGACATTTCTGACAGACTGGCCGCGTCT	2208
Qy	2810	CAGTGGACCTTCTAGTTTCAACAACAACAACAACAACAACAACAACAACAACAACAACA	2869
Db	2209	CTGTAGGACTTCCAGCT-----CAACAACAACAACAACAACAACAACAACAACAACA	2253
Qy	2870	TGGTTCAAAACAAAAGGAGACCCACAGTCAAGTGTGAAGTCTCTCTTATCTATCTATC	2929

Db 2254 CGGTCAACAAAGGACAGCCCAAGTCAGTGTGAACTGCTCCCTTTGTGCTC---TC 2310  
 QY 2930 ATTCCCAATTAATGTTTCCAGCCTTGTCACCCCTTTCTTCTACCCCATCTGTACAG 2989  
 Db 2311 ATGCTCAATTAATGTTTCCAGCCTTGTCACCCCTTTCTTCTACCCCATCTGTACAG 2367  
 QY 2990 CTGGCACTGCAACAGATGTCCTAAGCATAGACTTCAGGAGTTCAATCCCTGAGAAATAC 3049  
 Db 2368 -----CAGATATTTCTAAGCAGACAGCCCGGCAATTTGTTCCCTGCAAAATATC 2415  
 QY 3050 CTTCGCAATCTCTGCAACACAGCCGCAAGTTTCTTCTACAAATTCACAGAAATGTCGTG 3109  
 Db 2416 CTTCGCAATCTCTGCAACAGCCGCAAGTTTCTTCTACAAATTCACAGAAATGTCGTG 2475  
 QY 3110 AAAACAAAGACTCAGATTAATCTTCCCGCAGTCTTACTAGTCAGACACCTTCCCTCCA 3169  
 Db 2476 AACCCGAGACTCAGACAGCTCCCGCAGTCTTACTAGTCAGACACCTTCCCTCCA 2535  
 QY 3170 GTACATACAGAGGCAAGCCATCTAGACCTACCCGAGTAAATCAATGAACAGAGGAG 3229  
 Db 2536 GTACATACAGAGGCAAGCCATCTAGACCTACCCGAGTAAATCAATGAACAGAGGAG 2595  
 QY 3230 ATCCCTCAAAAAATAGCATGACACTTGTATGAACAGTATGCAATGTGATGACAGCT 3289  
 Db 2596 ACGCCACAAAAAGTAGCATGACACTTGTATGAACAGTATGCAATGTGATGACAGCT 2655  
 QY 3290 TTGGCTGTAGCAGCAATGACTAATGCTGTTATACCCAGTACGACAGACAGTGTACCC 3349  
 Db 2656 TTGGGCGCGCGGCAACAGTGTGCAACGCGCTCATCCCGACGACAGACAGTGTACCC 2715  
 QY 3350 CAGTAGAGGAGAAATGACATTAATGATGATGATGATGATGATGATGATGATGATGATG 3409  
 Db 2716 CAGTAGAGGAGAAATGACATTAATGATGATGATGATGATGATGATGATGATGATGATG 2775  
 QY 3410 TTCTTGAACCATCTATGCTTCAAGTATGATGATGATGATGATGATGATGATGATGATG 3469  
 Db 2776 TTCTTGAACCATCTATGCTTCAAGTATGATGATGATGATGATGATGATGATGATGATG 2835  
 QY 3470 TTCTTGTCT 3529  
 Db 2836 TTCTTGTCT 2895  
 QY 3530 AAAAGTGCAGAAAGATGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3589  
 Db 2896 AAAAGTGCAGAAAGATGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2955  
 QY 3590 TTCTCAGCGTCTCAGAGTGGCTTCCCATATGTTCTCAGCTGACAGTGTGAAGTGAAG 3649  
 Db 2956 TTCTCAGCGTCTCAGAGTGGCTTCCCATATGTTCTCAGCTGACAGTGTGAAGTGAAG 3015  
 QY 3650 ATATCATCTATTATTCACAGAGTACACAGACCTCTACAGAGCATACCAAGCAAAAC 3709  
 Db 3016 ATATTCATCTATTCACAGAGTACACAGACCTCTACAGAGCATACCAAGCAAAAC 3075  
 QY 3710 AACGTAATGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3769  
 Db 3076 AACGTAATGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3135  
 QY 3770 CTTCCTTGTATCAGGCTCAAGATGTGGAACTGAACTTTAAATGGCTGTTAAACAGTGA 3829  
 Db 3136 CTTCCTTGTATCAGGCTCAAGATGTGGAACTGAACTTTAAATGGCTGTTAAACAGTGA 3195  
 QY 3830 CTATATGTCAGAAACACATCTTCTGAGCAAGAAAGTACTAGACAGCTTAAAGAGAGAG 3889  
 Db 3196 CTATATGTCAGAAACACATCTTCTGAGCAAGAAAGTACTAGACAGCTTAAAGAGAGAG 3255  
 QY 3890 TAAAGATGATGAGGATCTGAATCATCCAAACATCTTGAATGTTGGAGGACAGGTG 3949  
 Db 3256 TAAAGATGATGAGGATCTGAATCATCCAAACATCTTGAATGTTGGAGGACAGGTG 3315  
 QY 3950 AGAAGAGCAATTTACATCTCTTCAATGAATGATGAGGAGGAGGATCGGTGCTCATTTGC 4009  
 Db 3316 AGAAGAGCAATTTACATCTCTTCAATGAATGATGAGGAGGAGGATCGGTGCTCATTTGC 3375

QY 4010 TGAGTAATATGAGGCTTTCAAAAGATCAGTACTATTACTACACTGACAGTACTCC 4069  
 Db 3376 TGAGTAATATGAGGCTTTCAAAAGATCAGTACTATTACTACACTGACAGTACTCC 3435  
 QY 4070 GTGGGCTTCTGATCTCCATGAAACCAAAATCATTCACAGAGATGTCAAAGTGGCAAT 4129  
 Db 3436 GTGGGCTTCTGATCTCCATGAAACCAAAATCATTCACAGAGATGTCAAAGTGGCAAT 3495  
 QY 4130 TGCTAATGACAGCACTGCTCAGAGACTAAGATGCAAGTATGCAAGTATGAGTGCAGCAG 4189  
 Db 3496 TGCTAATGACAGCACTGCTCAGAGACTAAGATGCAAGTATGCAAGTATGAGTGCAGCAG 3555  
 QY 4190 TGGCATCAAAAGAACTGCTGACAGAGATTTCAAGGACATTTACTGGGACATTTGCAT 4249  
 Db 3556 TGGCATCAAAAGAACTGCTGACAGAGATTTCAAGGACATTTACTGGGACATTTGCAT 3615  
 QY 4250 TTATGACATCAGGAGTACTAAGAGTCAACAGTATGGAAGAGGAGTGTATGAGAGT 4309  
 Db 3616 TTATGACATCAGGAGTACTAAGAGTCAACAGTATGGAAGAGGAGTGTATGAGAGT 3675  
 QY 4310 TTGGCTGTGCTATTATTAAGAAATGCGTGTGCAAAACACATGAGATGCAAGAAACACT 4369  
 Db 3676 TTGGCTGTGCTATTATTAAGAAATGCGTGTGCAAAACACATGAGATGCAAGAAACACT 3735  
 QY 4370 CCAATCATCTTCTTGTATTTAAAGATTGCTAGTGAACATCTGCTCCATCATGATCCTT 4429  
 Db 3736 CCAATCATCTTCTTGTATTTAAAGATTGCTAGTGAACATCTGCTCCATCATGATCCTT 3795  
 QY 4430 CACATTTCTCTCTGTTTGAAGAGATGCTGCTGCTGTTTGAAGATTCACACTGAG 4489  
 Db 3796 CACATTTCTCTCTGTTTGAAGAGATGCTGCTGCTGTTTGAAGATTCACACTGAG 3855  
 QY 4490 ACAGACCTCCATCAAGAGAGTACTGAACATCAGTCTTGTGACTACATGATGAG 4545  
 Db 3856 ACCGCGCTCGTCAAGAGAGTGTGTAACATCCGCTCTCGTGTGACAGAGTGTAG 3911

RESULT 10  
 AA079325  
 ID AA079325 standard; cDNA; 3260 BP.  
 XX  
 AC AA079325;  
 XX  
 DT 28-JUN-1995 (first entry)  
 XX  
 DE Mammalian MEK kinase (MEK 1) cDNA.  
 XX  
 KW MEK kinase; MEK 1; mitogen-activated protein kinase regulator;  
 KW MAPK; cell atrophy inhibition; Parkinson's; Alzheimer's; cancer;  
 KW autoimmune diseases; allergies; wound healing; oncogenes;  
 KW tumour agents; neurotrophic growth factor; ds.  
 XX  
 OS Mus musculus.  
 XX  
 FH key Location/Qualifiers  
 FT CDS 486..2504  
 FT /\*tag= a  
 PD WO9424159-A.  
 XX  
 PD 27-OCT-1994.  
 XX  
 PF 15-APR-1994; 94WO-US04178.  
 XX  
 PR 15-APR-1993; 93US-0049254.  
 XX  
 PA (NAE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.  
 PI Johnson GL;  
 XX  
 DR WPI: 1994-357747/44.  
 DR P-PSDB: AAR66029.

XX New MEK kinase protein and related antibodies and nucleic acid  
 PT regulator of mitogen activated protein kinase, useful  
 PT therapeutically to inhibit cell atrophy, to screen for oncogenes  
 etc.  
 XX  
 PS Claim 6; Page 8; 84pp; English.  
 CC  
 CC AA079325 encodes AAR6029 the mammalian MEK kinase (MEK 1), other  
 CC unique mammalian MEK kinases identified by PCR are described in  
 CC AAR6030 (MEK 2), AAR6031 (MEK 3) and AAR6032 (MEK 4). MEK is an  
 CC activator, independent of Raf protein, of mitogen-activated protein  
 CC kinases (MAPK). Inactivation of MEK can be used in the treatment  
 CC of some cancers, autoimmune diseases and allergies, while  
 CC stimulation can promote wound healing. MEK can also be used to  
 CC alleviate cellular atrophy in Parkinson's or Alzheimer's by acting  
 CC as a neurotrophic growth factor, and to screen for oncogenes and  
 CC tumour agents.  
 CC  
 XX  
 SO Sequence 3260 BP; 869 A; 837 C; 793 G; 761 T; 0 other;

Query Match 37.3%; Score 1955.6; DB 15; Length 3260;  
 Best Local Similarity 82.7%; Pred. No. 0;  
 Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

QY 1996 TATACCTCTTCCACAGTTTACGCGAAGAAATCAACTTCAGAGACTTTCACGCCAGTT 2055  
 DB 1 TACACTCTCTTCCACAGTTTACGCGAAGAAATCAACTTCAGAGACTTTCACGCCAGTT 60  
 QY 2056 GTAGACACATCTTCCAGTATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 2115  
 DB 61 GTAGACACATCTTCCAGTATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 119  
 QY 2116 TCAACACTGTGTGAAGTGTGCAAGAGCCAAAGCAGAGAGAGTGGCAGTTGGCAGAAATA 2175  
 DB 120 TCTACAGTGTGTGAAGTGTGCAAGAGCCAAAGCAGAGAGAGTGGCAGTTGGCAGAAATA 179  
 QY 2176 CTAAAGCTGTGATTCATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2235  
 DB 180 CTAAAGCTGTGATTCATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 239  
 QY 2236 AACCAACTGTGATTCATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2295  
 DB 240 AACCAACTGTGATTCATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 239  
 QY 2296 CTGTGTGTGAAGTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2355  
 DB 300 TTGCTGTGTGAAGTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 359  
 QY 2356 GCTGAGCTGTGATTCATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2415  
 DB 360 GCTGAGCTGTGATTCATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 419  
 QY 2416 TCCATTGATTAATCCAGTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2475  
 DB 420 TCCATTGATTAATCCAGTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 479  
 QY 2476 GCAAGAGTGTGTACAGTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2535  
 DB 480 GCGAGAGTGTGTACAGTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 539  
 QY 2536 TCCAGTGTGTACAGTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2595  
 DB 540 TCCAGTGTGTACAGTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 599  
 QY 2596 GAAATTTCCGAGAGTGTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2655  
 DB 600 GAAATTTCCGAGAGTGTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 658  
 QY 2656 TTCTTGAGAGCTGTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2715  
 DB 659 --CTTGAGAGCTGTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 707

QY 2716 TGCACAGTCCATTTAGAGAAACCTGGAAGAGATTAATGCTACAAAATTTAGTCCAGT 2775  
 DB 708 CACACAGTCCATTTAGAGAAACCTGGAAGAGATTAATGCTACAAAATTTAGTCCAGT 767  
 QY 2776 TCAGAGGACATTTCTGAGAGAGTGGCCAGATTCATGAGAGACCTTCTAGTCAACACA 2835  
 DB 768 TCAGAGGACATTTCTGAGAGAGTGGCCAGATTCATGAGAGACCTTCTAGTCAACACA 819  
 QY 2836 ACAAC 2895  
 DB 820 -----CAAC 872  
 QY 2896 AGTAGAGTTTGAAGTCTCTCTCTTATCTCATATTCATTCATTAATGTTTCCAGCTTG 2955  
 DB 873 AGTAGAGTTTGAAGTCTCTCTCTTATCTCATATTCATTCATTAATGTTTCCAGCTTG 929  
 QY 2956 TCAACCCCTTCT 3015  
 DB 930 TCAACCCCTTCT 974  
 QY 3016 CATAGACTTCAGAGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 3075  
 DB 975 CACAGACCCCGAGCATTTGTTCCCTGCAAAATACCTTCGCGATCTCTCTCTCTCTCTCT 1034  
 QY 3076 AAGTTTCTCTACAAATTCACAGAGAGTGTCTGTACACACAGAGTGTCTCTCTCT 3135  
 DB 1035 AAGTTTCTCTACAAATTCACAGAGAGTGTCTGTACACACAGAGTGTCTCTCTCT 1094  
 QY 3136 CCACTCTTCT 3195  
 DB 1095 CCACTCTTCT 1154  
 QY 3196 AGACCTACCCAGGATTAATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3255  
 DB 1155 AGACCTACCCAGGATTAATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1214  
 QY 3256 GATCTGAAGTATGTTTCAAAATGATGATGATGATGATGATGATGATGATGATGATG 3315  
 DB 1215 GATCTGAAGTATGTTTCAAAATGATGATGATGATGATGATGATGATGATGATGATG 1274  
 QY 3316 GCTGTATACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3375  
 DB 1275 GCTGTATACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1334  
 QY 3376 GTCAATACAGAGTCAACTCCAGTATGAGAGACCTTCTGAGAGATGATGATGATGAT 3435  
 DB 1335 GTCAATACAGAGTCAACTCCAGTATGAGAGACCTTCTGAGAGATGATGATGATGATG 1394  
 QY 3436 GATACACAGTATGTTTCAAAATGATGATGATGATGATGATGATGATGATGATGATG 3495  
 DB 1395 GATACACAGTATGTTTCAAAATGATGATGATGATGATGATGATGATGATGATGATG 1454  
 QY 3496 GATGATACCTTCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 3555  
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 QY 3556 GAAAGAGAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3615  
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 QY 3616 ATAGTCTCTACAGTGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3675  
 DB 1575 ATAGTCTCTACAGTGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1634  
 QY 3676 CCAGAGAGTATACAGAGATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3735  
 DB 1635 CCAGAGAGTATACAGAGATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1694  
 QY 3736 CTGAAGAGTCAAG 3795  
 DB 1695 CTGAAGAGTCAAG 1754  
 QY 3796 GGAACCTGGAATTAATGAGCTGTTAAACAGAGTGAATGATGATGATGATGATGATG 3855

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Db 1755 GGGACCTGGGACTTTAAATGGCTGTGMAACAGGTACGTACCTGAGAAACACATCTCCGAG 1814
QY 3856 CAAGAAGAAAGTACTAGAACACTAAGAGAGATAGAATGATGAGCCATCTGAATCAT 3915
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QY 3916 CCAAAATATCTTATGATGTTGGAGCCAGCTGTGAGAAAGCAATTAATCAATCTCTCAT 3975
Db 1875 CCAAAATATCTTATGATGTTGGAGCCAGCTGTGAGAAAGCAATTAATCAATCTCTCAT 1934
QY 3976 GAATGATGGCAGGAGATCGGTGCTCATTTGCTGAGTAATATGAGAGCTTCAAGAA 4035
Db 1935 GATGATGATGGCAGGAGATCGGTGCTCATTTGCTGAGTAATATGAGAGCTTCAAGAG 1994
QY 4036 TCAGTATGATTAATTAACATACATGAAAGCTTACTCCGTGGCTTGTATGATCAATGA 4095
Db 1995 TCAGTATGATTAATTAACATACATGAAAGCTTACTCCGTGGCTTGTATGATCAATGA 2054
QY 4096 CAATATCATTCACAGAGATGTCAAAGGTGCCAATTTGCTAATTAACAGCAGCTGTGAGA 4155
Db 2055 CAGATATTCACAGAGATGTCAAAGGTGCCAATTTGCTAATTAACAGCAGCTGTGAGA 2114
QY 4156 CTAGAATTCACAGATTTTGGAGCTGCAGCCAGGTGGCATCAAAAGAACTGGTGACAGA 4215
Db 2115 CTAGAATTCACAGATTTTGGAGCTGCAGCCAGGTGGCATCAAAAGAACTGGTGACAGA 2174
QY 4216 GACTTTTCAGGGACAAATTAATGAGGACAAATTCATTAATGAGCAGTACTAGAGAT 4275
Db 2175 GACTTTTCAGGGACAAATTAATGAGGACAAATTCATTAATGAGCAGTACTAGAGAT 2234
QY 4276 CACACATATGAGAGAGAGCTGTGATGATGAGAGTGTGGCTGTCTTATGAATAGCT 4335
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QY 4336 TGTGCAAAACACACATGAGATGAGAAAAACACTCCATCATCTTGTGATTAATTAAG 4395
Db 2295 TGTGCAAAACACACATGAGATGAGAAAAACACTCCATCATCTTGTGATTAATTAAG 2354
QY 4396 AATGTAATGCAACTCTGCTCCATGATCCCTTACATTTGCTCTGTTTACAGAGAT 4455
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QY 4456 GTGGCTCTTCGTTGTTTAACCTCACTCAGAGACAGCTCCATCAAGAGAGCTACTG 4515
Db 2415 GTGGCTCTTCGTTGTTTAACCTCACTCAGAGACAGCTCCATCAAGAGAGCTACTG 2474
QY 4516 AAGCATCAGTCTTGTCTACTACATGATGATGATGATGATGATGATGATGATGATGAT 4575
Db 2475 AAGCATCAGTCTTGTCTACTACATGATGATGATGATGATGATGATGATGATGATGAT 2534
QY 4576 AGGATGCTCAACAGAGAAAAAACTTG---TGGGGAACCATTTGATTAATCTGAG 4631
Db 2535 AGGATGCTCAACAGAGAAAAAACTTG---TGGGGAACCATTTGATTAATCTGAG 2594
QY 4632 CCATGATGCTCAGTAACACTATGAAAGAGGCAAGTGGGGAACCTTACTAGATGATG 4691
Db 2595 CCATGATGCTCAGTAACACTATGAAAGAGGCAAGTGGGGAACCTTACTAGATGATG 2653
QY 4692 AATGCAAAATCATGATCTTACTTACATGATGATGATGATGATGATGATGATGATGATG 4750
Db 2654 AATGCAAAATCATGATCTTACTTACATGATGATGATGATGATGATGATGATGATGATG 2713
QY 4751 ACTGTAAGTGTGCTTTTCAAGAACTGGCTTAGGTGAACAGAAACAAATGAAGTTTG 4810
Db 2714 ACTGTAAGTGTGCTTTTCAAGAACTGGCTTAGGTGAACAGAAACAAATGAAGTTTG 2773
QY 4811 CATGACTAATATGAGAGACATTAATTTTATTTTGGAGCACTTTTACAGAA 4864
Db 2774 CATGACTAATATGAGAGACATTAATTTTATTTTGGAGCACTTTTACAGCA 2825

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AAV22676
ID AAV22676 standard; cDNA; 3260 BP.
XX
AC AAV22676;
XX
DT 17-JUL-1998 (first entry)
XX
DE cDNA encoding a murine mitogen-activated protein kinase kinase (MAPKK).
XX
KW Mitogen-activated protein kinase kinase; MAPKK; mouse;
KW extracellular signal-regulated kinase kinase; MEKK; regulation;
KW signal transduction; raf-independent arm; screening assay; treatment;
KW disorder; cancer; autoimmune disease; inflammation; allergy;
KW neuronal disease; Parkinson's disease; Alzheimer's disease; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..485
FT CDS /*tag= a
FT /*tag= b
FT 3'UTR 2502..3260
FT /*tag= c
XX
PN US5753446-A.
XX
PD 19-MAY-1998.
XX
PF 06-JUN-1995; 9505-0472934.
XX
PR 15-APR-1993; 9305-0049254.
PR 14-OCT-1994; 9405-0323460.
PR 21-FEB-1995; 9505-0354516.
PR 12-MAY-1995; 9505-0440421.
XX
PA (MABE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Johnson GL;
XX
DR MPI; 1998-111395/27.
DR P-PSDB; AAM56157.
XX
PT Screening assay for regulators of MEKK signal transduction - using
XX mammalian MEKK polypeptide
XX
PS Claim 6; Columns 29-34; 48bp; English.
XX
CC The present sequence encodes a murine mitogen-activated protein kinase
CC kinase (MAPKK) (also known as extracellular signal-regulated kinase
CC kinase (MEKK)). The protein, which is serine/threonine kinase is capable
CC of regulating signal transduction in cells. It regulates the activity of
CC elements of the raf-independent arm of MEKK. A screening assay for
CC compounds that regulate signal transduction by a MEKK protein complex
CC contacting a reaction mixture containing a mammalian MEKK polypeptide and
CC a test compound and determining the effect of the test compound on an
CC indicator of signal transduction by the MEKK polypeptide in the reaction
CC mixture. Compounds identified by the above assay can be used to prepare
CC therapeutic compositions for treating disorders that are subject to
CC regulation or cure by manipulating a signal transduction pathway in
CC cells involved in the disorders, e.g. cancer, autoimmune diseases,
CC inflammations, allergies, and neuronal diseases such as Parkinson's
CC disease and Alzheimer's disease.
XX
SO Sequence 3260 BP; 869 A; 837 C; 793 G; 761 T; 0 other;
XX
Query Match 37.3%; Score 1955.6; DB 19; Length 3260;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;
QY 1996 TATACCTCTTGGCAGAGTTAGCGGAAGATCAAACTTCAAGAGCTCTCCAGCCAGTT 2055
Db 1 TACACTCTTGGCAGAGCTGTGGAGAAAGATCAAACTTCAAGAGCTCTCCAGCCAGTT 60

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QY	2056	GTAAACACATCTCTAGTCAAAATGTGCAGATGCCATATGCCGACAAAGTCAGCTGTCCATA	2115
Db	61	GTAAACACTATTCCTGTGCAAGTGTGCAGAT--CCAACAGCCGACCAAGTCACCTGTCCATA	119
QY	2116	TCAACATCTGTGGAACTGTGTCCAAAGGCCCAAGACAGAGAGATTTGGCAGTTGGCAGAAATA	2175
Db	120	TCATACATGTGTGAATCTCTCAAGGGCCCAAGCAGAGAGACTGGCGTTGGAGAAATA	179
QY	2176	CTAAAAGCTGGATCCATTTGGTATTTGGTGTGTGATTATGTCTAAATTTGATTTCTTGGGA	2235
Db	180	CTTAAAGCTGGGTCCATTCGGGGTGTGGTGTGTGCTGATTAAGCTTAAGTTGATCTTTGGA	239
QY	2236	AACCAAACTGAATCAAAACATTGGCAAGAACTCTTTGGCGCCCTTGTCTTAATAGATTA	2295
Db	240	AACCAACCTGAATCAAAACCTGGCAAGAACTGTGGGTGCGCTGTCTTATTAAGACAGG	299
QY	2296	CTGTGTGTGGAAATTCCTGCTGATGAATTTATTCCTCATATTTGTCAGTACAGATGTTTCCAA	2355
Db	300	TTGCTGTGGAAATTCCTGCTGATGAATTTCTATTCCTCATATTTGTCAGTACAGATGTTTCCAA	359
QY	2356	GCTGAGCCTGTGAAATCAGGTTAAAGAGCTGTCTCCCTTTAACTTTGCTTTGCGAG	2415
Db	360	GCTGAGCCTGTGAAATCAGGTTCAAGAAAGCTGTCTCCCTTTAACTTTGCTTTGCGAA	419
QY	2416	TCCATTTGATTAATTCGCCCACTAATGTTGGCAAACTTTCCAGAAAGATCTACTGTAGTCT	2475
Db	420	TCCATTTGATTAATTCGCCCACTAATGTTGGCAAACTTTCCAGAAAGATCTACTGTAGTCT	479
QY	2476	GCAAGAAATGTTACTATACAGTACGATCCCATGTGTGTTTCAAAACGTGTAAATGCTGAGT	2535
Db	480	GCCAGGATGTTGTGACCGGACAGTGGCCGCTGTGTGTTTCCAACTGTAAACATGTTATGCT	539
QY	2536	TTCAGTTTCCACTACTACCTACACAGAGATGGCGGCGTTTATGTCGATTTGAGATGAGGTG	2595
Db	540	TTTGCGCTCCACCACTTCCACAGAGATGGCGGCGCTGTATGCTATGCGGATGAGGTA	599
QY	2596	GAATTTGCCGAAGCCATCCAGTTGGCGGTAGAAGACATTTGGATGTCACAGAGACAGC	2655
Db	600	GAATTTGCCGAGGTCATCCAGTGTGGGTGAGAGACACTGTGATTTGGGATCAGGACAG-	658
QY	2656	TTTCTGGAGGATCTGTGTCCCAACACTATCTGTGAAACACAGAAACAGTTCCTCCCTAG	2715
Db	659	--CTTAAAGGCGGTGGCCCCCACCACTGTCT-----AGAAACAGCTCCCTTTAG	707
QY	2716	TGCACATCTCATTTAGAGAAATCTGAAAAAGATTATGTCTACAAAAATTGAGTCCAGT	2775
Db	708	CACACATCTCATTTAGAGAAATCTGAAAAAGACTAAGTCTACAGACTAGTGTCCAGC	767
QY	2776	TCAGAGACATTTCTGAGAGACTGGCCAGCATTTCTAGTAGACCTTTAGTTCAACAACA	2835
Db	768	TCGAGAGACATTTCTGACACACTGGCCGCGCTCTGTGTAGGACTTCCACAGCT-----	819
QY	2836	ACAACAACAACAACAAGAGCAACCAAAAGCCAAATGGTTCAAAACAAAAGGACAGCCAGC	2895
Db	820	-----CAACAACAACAACAACAACCAAGCCAGGCTTTCAAAACAAAAGGACAGCCAC	872
QY	2896	AGTCAGTGTTTGAATCTCTCTCCCTTATCTCATCATTTCCCAATTATGTTCACACCTTG	2955
Db	873	AGTCAGTGTTTGAATCTCTCTCCCTTGTGTC--TCAGTCTCAATTTATGTTCACACACCA	929
QY	2956	TCAACCCCTTCTTCTTCTAACCATCTGTACCAAGCTGGCACTGGCAACAGATGTCTTAAG	3015
Db	930	TCACCCCTTGTCTCTCTGTGCCCTGTGTCTC-----CAGATATTTCTTAAG	974
QY	3016	CATGAGCTTGAAGGATTCATTTCCCTCCAGAAATACCTTTCGATCTCTCAACACAGAGGC	3075
Db	975	CACAGACCCAGGATTTGTTCCTCGAAAAATACCTTCGCACTCTCTCAGACACAGGCG	1034
QY	3076	AAGTTTCTCTACAAATTCACAGAAACTGTCTGAAAACAAAAGCTCAGATTAACCTTTCC	3135
Db	1035	AAGTTTCTCTACAAATTCACAGAACTGTCTGAAACACGAGACTCAGACACGCTCTCC	1094

OY	3136	CCAGTCTTTACTAGTCAGTCAAGACCCCTTGCCCTCAGTACATACAGGCCAAAGCATCT	3135
OY	3136		
Db	1095	CCAGTCTTCACTAGTCAAGTCAAGCCCAACCTCCAGTAACTACAGGCCAAAGCATCC	1154
OY	3196	AGACCTTACCAGGTATATACAGTAAACAGGGGAGATCCCTCAAAAATAATGCATGCATCT	3255
Db	1155		
OY	3256	GATCTGAACAGTATAGTTCGCAATATGTGATGACAGCTTGGCTGTAGCAGCAATAGTAT	3315
Db	1215		
OY	3316	GCTGTATTACCCAGTGCAGACAGTGTTCACCACAGTACAGAGAGAAATGCAGATTAGAT	3375
Db	1275		
OY	3376	GTCATATACAGGTCACACCTCAGTATTTGGAGGACCTTGTGAAGCACTATAGCTCTTCAAGT	3435
Db	1335		
OY	3436	GATACACAGTAACTTTTAACTGAGAGAGTGTGCTGCTCTCTCGTAAAAAGGCTGAAT	3495
Db	1395		
OY	3496	GATGATACCTTACAAAGATGATGTGAATCATATATCAAAAAGTGCAGAGAGAGATGAGACT	3555
Db	1455		
OY	3556	GAACAGAGAGAGGCTTTAGGAAATTTGCCATNGGCAATGTCAAGCTCTCAGAGTATGCCCTCCCC	3615
Db	1515		
OY	3616	ATATGTCCTCAGCTGCAGGTTTGAATAATGAGAGATATCATATTTTCAACAGATATACA	3675
Db	1575		
OY	3676	CCAGAGACTCTACAGGACATACCCAAAGCAAAACGATATAGAGAAAGACATGATATGG	3735
Db	1635		
OY	3736	CTGAAGAGTCAACAGATAGAGGCTTTGGAGCATTTTCTTCTGTATATCAGGCTCAAGATGTG	3795
Db	1695		
OY	3796	GGAATCGGAATTTAAATGCGCTGTTTAAACAGAGTACTATATGTAGAGAAACATCTTCTAG	3855
Db	1755		
OY	3856	CAAGAGAGATAGTAGAAGCACTAAGAGAAAGAGATTAAGATGATAGGCATCTGATATCAT	3915
Db	1815		
OY	3916	CCAAACATCATTAGAGATGTTGGGAGGCCAGCTGTGAGAAAGCAATATCATCTCTTCACTT	3975
Db	1875		
OY	3976	GAATGGATGGCAGGGGAGTGGTGGCTCAATTTGCTAGTAAATTAATGGAGCCCTTCAAAATA	4035
Db	1935		
OY	4036	TCAGTAGTTATTAATCACTACCTGAAACAGTTACTCCGTGGCCTTTCGATATCTCCATGAATAC	4095
Db	1995		
OY	4096	CAATCATTTACAGAGATGTCCAAAGGTGCCAATTTCTTAATTGACAGCACTGTGTACAGCA	4155
Db	2055		
OY	4156	CTAAGAAATTCAGATTTTTTGGAGCTGCAGGCCAGGTTGGCATCAAAAAGAGAACTGTGCACAGA	4215
Db	2115		
OY	4216	GAGTTTACGGCACAAATTTCTGGGGACAAATTTGCAATTTATGTGCACTGTAGGTACTAAGAGAT	4275







Dh 659 --CTTACAGGCGCTGGCCCCACCACGCTGTCT-----AGAAAACAGCTCCCTTGAG 707  
Qy 2716 TGCACAGTCCATTTAGAGAAACTGGAAGAGATATATGCTCTACAAAATTGAGTGCAGT 2715  
Dh 708 CACACAGTCCATAGAGAAACTGGAAGAGATATATGCTCTACAAAATTGAGTGCAGT 767  
Qy 2776 TCGAGAGACATTTCTGAGAGACTGCGCAGCATTTCACTAGAGACCTTCTAGTCAACACA 2835  
Dh 768 TCGAGAGACATTTCTGAGAGACTGCGCAGCATTTCTAGAGACTTCCACCT----- 819  
Qy 2836 ACAACACACACACACAGAGACACCAAGCCAAATGGTTCAAAACAAAAGGAGACCCAC 2895  
Dh 820 -----CAACAAACACACACACACCAAGCCAGGCTTAAACAAAAGGAGACCCAC 872  
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Dh 1035 AAGTTTCTCTACAAATTCACAGAAACTGTCTGAAAACAAGACAGATCAATTAATCTTCC 1094  
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Dh 1335 GTCATATACAGAGTCAACAGTATGAGAGACCTCTCTGAAGATATGAGCTTCAAGT 1394  
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Dh 1395 GATACACACAGTATGTCACAAATGTGATGACAGCTTGTGCTGTGAAAAGGCTGAAAT 1454  
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Dh 1455 GATGATACCTACAAAGATGATGATCATATCAAAATGTCAAAAGAGAGATGAAAGT 1514  
Qy 3556 GAG 3615  
Dh 1515 GAG 1574  
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Dh 1695 CTGAAAGGTCACAGATAGAGCTTGGAGCATTTTCTTCTGTTTACAGAGCTCAAGATGTG 1754

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Qy 3856 CAGAGAGAGTATAGAGACCTTAAGAGAGAGATTAAGATATGATGAGCATCTAATCAT 3915  
Dh 1815 CAGAGAGAGTATAGAGACCTTGAAGGAGAGATCCGAGATGAAGTGGGTCACCTCAACCAT 1874  
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Qy 3976 GAATGATGCGAGGAGGATCGGTGGCTCATTTGCTGAGTAATATGAGCCCTTCAAGAA 4035  
Dh 1935 GATGATGCGAGGAGGATCGGTGGCTCATTTGCTGAGTAATATGAGCCCTTCAAGAG 1994  
Qy 4036 TCACTAGTATTAATACATACAGTAACTACTCCGTGGCTTTGCTGATCTCATGAAAC 4095  
Dh 1995 TCACTAGTATTAATACATACAGTAACTACTCCGTGGCTTTGCTGATCTCATGAAAC 2054  
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Dh 2055 CAAATCATATACAGAGATGCAAGAGTCAAGAGTCAATTTGCTAATGACAGACGTGCAGAG 2114  
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Dh 2175 GAGTTTCAAGGACATTAATCTGAGGACATTCATATTTATGACACCTGAGATCTAAGAGT 2234  
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 KW allergic response; neuronal disorder; Parkinson's disease;  
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 XX  
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 AC AAL41577;  
 XX 19-APR-2002 (first entry)  
 DE Murine MEK1-1 coding sequence.  
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 KW Mouse; MEK1; mitogen ERK kinase; enzyme; cancer; neuroprotective;  
 KW auto-immune disease; signal transduction; allergy; inflammation;  
 KW neurological disorder; hormone-related disease; apoptosis; infection;  
 KW cytosolic; immunosuppressive; anti-inflammatory; antiallergic; gene;  
 KW nototropic; antiparkinsonian; contraceptive; ss.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT CDS 486..2504  
 FT /\*tag= a  
 FT /product= "MEK1.1"  
 PN US6333170-B1.  
 XX 25-DEC-2001.  
 PD 05-APR-1996; 96US-0628829.  
 PF 15-APR-1993; 93US-0049254.  
 PR 14-OCT-1994; 94US-0323460.  
 PR 12-MAY-1995; 95US-0440421.  
 PR 06-JUN-1995; 95US-0472934.  
 PA (NAJF-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.  
 PI Johnson GL;  
 DR WPI: 2002-163179/21.  
 DR P-PSDB; AAM48934.  
 PT New isolated nucleic acid encoding mitogen extracellular  
 PT signal-regulated kinase kinase, useful for gene therapy of e.g. cancer  
 PT and for recombinant protein production  
 XX  
 PS Claim 1; Column 101-108; 125pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of a  
 CC number of murine mitogen extracellular signal-regulated kinase (ERK)  
 CC kinase kinase (MEK) enzymes. The sequences can be used to treat a wide  
 CC range of diseases including cancer, autoimmune diseases, inflammation,  
 CC allergies, degenerative neurological diseases and hormone-related  
 CC diseases, and for inhibiting spermatogenesis or oocyte maturation for  
 CC contraception. The present sequence is the murine MEK1.1 coding  
 CC sequence.  
 XX  
 SQ Sequence 3260 BP; 869 A; 837 C; 793 G; 761 T; 0 other;  
 Query Match 37.3%; Score 1955.6; DB 24; Length 3260;  
 Best Local Similarity 82.7%; Pred. No. 0;  
 Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;  
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 Db 1 TACACTCTTGTGCGCAGATTTGAGAGAGATGCAATCTGAGAGATCTTCCAGCAGTT 60

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Db	61	GTAGACATATTCCTTGTCCAAGTGTGCAGAT - CCACAGCCGACAGTACGTGTCCATA	119
OY	2116	TCAACACTGTGGAACGTGTGCAAAGGCCAAGCGAGAGTGTGGCAGTTGGCGAGAAATA	2175
Db	120	TCTACAGTGTGGAACACTGTGCMAAGGCCAAGCGAGAGTGTGGCGAGAAATA	179
OY	2176	CTAAAAGCTGATCCATTTGGTATTGGTGTGTGATTATGTCTTAAATGTATTCTTGG	2235
Db	180	CTTAAAGCTGGGTCATCGGGGTTGGGTGTGATTTACGTCTTAAGTTGTATCCTTGG	239
OY	2236	AACCAACTGAAATCAACATTTGGCAAGACTCTTGGCCGCTTGTCTTATAGATAGA	2295
Db	240	AACCAAGCTGAAATCAACACTGGCAAGAACTGTGGTGCTGTCTTATATAGCAGG	299
OY	2296	CTGTGTGTGCAATTTCCGTGTGAATTTTATCCCATTTGTGAGTACAGATGTTTCAAC	2355
Db	300	TTCGCTGTGGAATTTCCGTGTGAATTTCTATCCCATATTGTACAGTGTGTCTACAA	359
OY	2336	GCTAGACCTGTGGAATCAGGTAATAAGACTGTCTGCCCTTAACTTATCTTGGCAG	2415
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OY	2416	TCCAAATGATATTCGCCATCCTCAATGTGTGGCAAACTTCCAGAAGATCTACTAGTTC	2475
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Db	540	TCTGTGCTCACCCACTTCACACAGAGTGTGCCGCTGTGTATGGCTATGCGAGTAGGTA	599
OY	2596	GAAATTCGCCAAGGCAATCCAGTGTGGCGGTAGAAGACACTTTGGATGTGCAACAGACG	2655
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Db	659	- -CTTACAGGCGCGTGGCCGCCACACACTGTCT - -AGAAACAGCTCCCTTGAG	707
OY	2716	TGCACATCCATTTAAGAGAAACTGGAAGAAATTTATGTGTACAAATTTGATGTCCAGT	2775
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Search completed: December 27, 2002, 16:58:43  
 Job time : 1028 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 20, 2002, 16:20:44 ; Search time 32 Seconds

(without alignments)  
4542.351 Million cell updates/sec

Title: US-09-697-898-2

Perfect score: 7825

Sequence: 1 MAAAGNRASSSGFPGARAT.....PDNRPPRELLKHPVRRITW 1512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6892.5	88.1	1493	2 T10757	MAP kinase kinase
2	3172.5	40.5	687	2 A46212	MEK kinase - mouse
3	619	7.9	1478	2 S20117	protein kinase BCK
4	595.5	7.6	706	2 A48084	STREII protein kina
5	591.5	7.6	651	2 A96591	NPK1-related prote
6	552.5	7.1	1338	2 T30565	MAP kinase kinase
7	543.5	6.9	659	1 A39723	protein kinase byr
8	538.5	6.9	883	2 A96662	hypothetical prote
9	535	6.8	738	1 S51380	protein kinase STE
10	531.5	6.8	608	2 G96575	probable MEK kinas
11	517.5	6.6	1116	2 T38073	serine/threonine-p
12	502.5	6.4	1607	2 T03022	MAP kinase kinase
13	484	6.2	652	2 H86221	hypothetical prote
14	483	6.2	582	2 T51625	MAP3k alpha protei
15	461.5	5.9	608	2 T01833	serine/threonine-s
16	455.5	5.8	650	2 JC4673	protein kinase (EC
17	449.5	5.7	535	2 T51736	mitogen-activated
18	447	5.7	773	2 T01835	serine/threonine-s
19	446	5.7	372	2 T52621	mitogen-activated
20	445.5	5.7	560	2 D85084	probable mitogen-a
21	436.5	5.6	572	2 T01836	serine/threonine-s
22	433.5	5.5	1401	2 T39225	MAP kinase kinase
23	429.5	5.5	1379	2 JC5778	apoptosis signal-r
24	426	5.4	560	2 T14616	hypothetical prote
25	423	5.4	372	2 T02350	NPK1-related prote
26	423	5.4	1579	2 S59801	protein kinase SSK
27	415	5.3	1387	2 T16511	hypothetical prote
28	413.5	5.3	1288	2 JE0363	mitogen-activated
29	410	5.2	836	2 B96716	probable serine/th

30	409.5	5.2	1895	2 T06609	disease resistance
31	399	5.1	471	2 T39232	probable serine th
32	398.5	5.1	658	2 T39500	serine/threonine-s
33	392	5.0	756	2 T50298	MAP kinase kinase
34	389.5	5.0	403	2 JC5974	aurora-related kin
35	388.5	5.0	939	2 S28394	probable serine/th
36	385	4.9	525	2 S58682	protein kinase, p2
37	380.5	4.9	339	2 C86185	hypothetical prote
38	380.5	4.9	658	2 S60170	protein kinase Pak
39	377.5	4.8	544	2 A57597	beta-p21-activated
40	377.5	4.8	544	2 S40482	serine/threonine-s
41	377.5	4.8	545	2 G01773	p21-activated prot
42	377.5	4.8	1418	2 T15232	hypothetical prote
43	373.5	4.8	1062	2 S46367	protein kinase CDC
44	373.5	4.8	1230	2 T18259	serine/threonine p
45	373	4.8	1230	2 T18256	probable serine/th

ALIGNMENTS

RESULT 1

T10757

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jul-1999 #sequence: revision 16-Jul-1999 #text: change 21-Jul-2000

C:Accession: T10757

R:Yu, S.; Robbins, D.J.; Christerson, L.B.; English, J.M.; Vanderbilt, C.A.; Cobb, M.

Proc. Natl. Acad. Sci. U.S.A. 93, 5291-5295, 1996

A:Title: Cloning of rat MEK kinase 1 cDNA reveals an endogenous membrane-associated 1

A:Reference number: Z17123; MUID:96224276; PMID:8643568

A:Accession: T10757

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1493 <XUS>

A:Cross-references: EMBL:U48596; NID:q1354136; PID:NAC52596.1; PID:q1354137

C:Genetics:

A:Gene: MEK1

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C:Keywords: ATP; phosphotransferase; protein kinase

Query Match	88.1%	Score 6892.5	DB 2	Length 1493
Best local similarity	89.2%	Pred. No. 7e-232		
Matches 1350; Conservative 45; Mismatches 96; Indels 23; Gaps 8;				
Qy	1	MAAAGNRASSSGFPGARATSPBAGGGGALKASSAPAAAGILREAGSGGERADWRR	60	
Db	1	MAAAGNRASSSGFPGARATSPBAGGGGALKASSAPAAAGILREAGSGGERADWRR	60	
Qy	61	QLRKRVSELDOLPEQPLFLAASPASTSPSPBPADAAGSGTGFPYAVPPHGAASRG	120	
Db	61	QLRKRVSELDOLPEQPLFLAASPASTSPSPBPADAAGSGTGFPYAVPPHGAASRG	120	
Qy	121	GAHLTESVAAPDSGASPPAAAPGEGKRAPAEPSPAAAPGEMENKFTGLHMDRP	180	
Db	121	GAHLTESVAAPDSGASPPAAAPGEGKRAPAEPSPAAAPGEMENKFTGLHMDRP	180	
Qy	181	EEEMIREKLAKTQMPAMKHEWLERRRNRGPVYKPIPAKGDSSENNHDLAESPGEVQASA	240	
Db	171	EEEMIREKLAKTQMPAMKHEWLERRRNRGPVYKPIPAKGDSSENNHDLAESPGEVQASA	230	
Qy	241	ASPASKGRSPSPGNSPGSGRTVKSSEPGVRRKRVSPVPOSGRTIPPRAPSPDGFSPYS	300	
Db	221	AAAPAKGRSPSPGNSPGSGRTVKSSEPGVRRKRVSPVPOSGRTIPPRAPSPDGFSPYS	290	
Qy	301	PEETRRVNVKVARLYLTLQIGPNSFLIGGSPNKKRVFPGPONGSCARPTGTHLLF	360	
Db	291	PEETRRVNVKVARLYLTLQIGPNSFLIGGSPNKKRVFPGPONGSCARPTGTHLLF	350	
Qy	361	VMLRVQLEPSPDMLRKTLEKFEVESLFQKXHSRRSSRIKAPSRNTLOKEVSRASNSHT	420	
Db	351	VMLRVQLEPSPDMLRKTLEKFEVESLFQKXHSRRSSRIKAPSRNTLOKEVSRASNSHT	410	

QY 421 LSSSTSTSSNSIKDEEOMCPTICLLGMDDEESTVCEDCGRNKLHHHCSINAEBCR 480  
DB 411 LSSSTSTSSNSIKDEEOMCPTICLLGMDDEESTVCEDCGRNKLHHHCSINAEBCR 470  
QY 481 RRREPLICPLCKSKMRSHDFYGHESLSPVDSPLRAAQQOQVQOOLPAGS--RRQESNF 539  
DB 471 RRREPLICPLCKSKMRSHDFYGHESLSPVDSPLRLGVOQPSPOQVAGSQRRQESNF 530  
QY 540 NLTHVGTQOIPPAYKDLAPWIQVEGMELVGLFSNNMVRREMLARRLSHDVSGALLLAN 599  
DB 531 NLTHVGTQOIPPAYKDLAPWIOAFGMELVGLFSNNMVRREMLARRLSHDVSGALLLAN 590  
QY 600 GSGTSGSSSSSSSGSGATSGSSQTSISGDVVEACCSYLTMWCADPYKVVYAAKTKLR 659  
DB 591 GSGTSGSSSSSSSGSAGASSSSQTSISGDVVEACCSYLTMWCADPYKVVYAAKTKLR 650  
QY 660 AMLVYTPCHSLAEIKLQRLQPVDTILVKCADANSRTQSISITLLELCKGQAGELAV 719  
DB 651 AMLVYTPCHSLAEIKLQRLQPVDTILVKCADANSRTQSISITLLELCKGQAGELAV 710  
QY 720 GREILKAGSIGIGVDVYVNCILGNOTESNNQELIGRLCLIDRLLEFPAEYPHIVST 779  
DB 711 GREILKAGSIGIGVDVYVNCILGNOTESNNQELIGRLCLIDRLLEFPAEYPHIVST 770  
QY 780 DYSOAEPIVIRKKLILTLFALQSIDNSHSMWGLSRRIYLSNARMYTPVHVESKLE 839  
DB 771 DYSOAEPIVIRKKLILTLFALQSIDNSHSMWGLSRRIYLSNARMYTPVHVESKLE 830  
QY 840 MLVSSSTHTFTMRRLMAIADEVEIAEAIQGVEDTLDGQODSFLQASVPPNNYLETTEN 899  
DB 831 MLVSSSTHTFTMRRLMAIADEVEIAEAIQGVEDTLDGQODSFLQASVPPNNYLETTEN 886  
QY 900 SPECTVHLKTKGKICATKLSASSEDISERLASISVG--PSSSTTTTTTTTTTQOPKPMVOT 958  
DB 887 SPECTVHLKTKGKICATKLSASSEDISERLASISVG--PSSSTTTTTTTTTTQOPKPMVOT 940  
QY 959 KRRPSQCNSSPLSHHSQMLFPALESTPSSSTPSVPAGTATYQSKRLGQIFPCRIPLSAS 1018  
DB 941 KRRPSQCNSSPLSHHSQMLFPALESTPSSSTPSVPAGTATYQSKRLGQIFPCRIPLSAS 999  
QY 1019 POTOGRFSLQFHRNCPENKSDKLSFVQSPRLPSSNHRPKPSRPTPGNTSKOGDPAK 1078  
DB 1000 POTOGRFSLQFHRNCPENKSDKLSFVQSPRLPSSNHRPKPSRPTPGNTSKOGDPAK 1059  
QY 1079 NSMTLDLNSSSKCDSPGCCSSNSNAVIPSDETFTPVBEKCRDLVNTLNSIEDLLEA 1138  
DB 1060 NSMTLDLNSASQCDSPGCCSSNSNAVIPSDETFTPVBEKCRDLVNTLNSIEDLLEA 1119  
QY 1139 SNPSSDTVTYFKSEYAVLSPKAEKNDYTKDDVNNHOKCKEKMEAEFEALAIAMAMAS 1198  
DB 1120 SNPSSDTVTYFKSEYAVLSPKAEKNDYTKDDVNNHOKCKEKMEAEFEALAIAMAMAS 1179  
QY 1199 ODALPITVPOLOVENGEDIIIIQODTPETLPGHTKAKOPYREDTBMKGOQIGLAFSSCY 1258  
DB 1180 ODALPITVPOLOVENGEDIIIIQODTPETLPGHTKANEPRREDTBMKGOQIGLAFSSCY 1239  
QY 1259 QAOQVGTGLMAVKQVTVRNTSSBOEYVEALREIRIMASHLNHPNIIIRMLGATEKSN 1318  
DB 1240 QAOQVGTGLMAVKQVTVRNTSSBOEYVEALREIRIMASHLNHPNIIIRMLGATEKSN 1299  
QY 1319 YMLFETEMMAGSAVHLSTYGAFFKESVINYTEQOLRGLSTYHENOIIHRDVGANLLID 1378  
DB 1300 YMLFETEMMAGSAVHLSTYGAFFKESVINYTEQOLRGLSTYHENOIIHRDVGANLLID 1359  
QY 1379 STGQRLRIADFGAARLASKGTGAGFQQLGTTAFMAPEVLRGOOYGRSCDWMVSGCA 1438  
DB 1360 STGQRLRIADFGAARLASKGTGAGFQQLGTTAFMAPEVLRGOOYGRSCDWMVSGCA 1419  
QY 1439 IIEMACAKPNNAEKSHNLALIFKIASATVAPSTPSHLSPEGLRDVALRCLLEIOPDRPP 1498  
DB 1420 IIEMACAKPNNAEKSHNLALIFKIASATVAPSTPSHLSPEGLRDVALRCLLEIOPDRPP 1479  
QY 1499 SRELLKHVFRRTTW 1512

DB 1480 SRELLKHVFRRTTW 1493  
RESULT 2  
A46212  
MEK kinase - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-May-1999  
C:Accession: A46212  
R:Range-Carter, C.A.; Pleieman, C.M.; Gardner, A.M.; Blumer, K.J.; Johnson, G.L.  
Science 260, 315-319, 1993  
A:Title: A divergence in the MAP kinase regulatory network defined by MEK kinase and  
A:Reference number: A46212; M01D:93227040; PMID:8385802  
A:Accession: A46212  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-687 <L>A>  
A:Experimental source: brain  
A>Note: sequence extracted from NCBI backbone (NCBIP:129292)  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom  
C:Keywords: ATP  
F:416-683/Domain: protein kinase homology <KIN>  
F:424-432/Region: protein kinase ATP-binding motif  
Query Match 40.5%; Score 3172.5; DB 2: Length 687;  
Best Local Similarity 89.5%; Pred. No. 2,4e-103;  
Matches 628; Conservative 21; Mismatches 38; Indels 15; Gaps 5;  
QY 811 MYGKLSRRILYLSABRMYTVPHVFSKLEMLSVSSSTHTFRRRRRLMAIADVEIAEATO 870  
DB 1 MYGKLSRRILYLSABRMYTVPHVFSKLEMLSVSSSTHTFRRRRRLMAIADVEIAEATO 60  
QY 871 LGVEDTLDGQODSFLQASVPPNNYLETTESSPECTVHLKTKGKICATKLSASSEDISER 930  
DB 61 LGVEDTLDGQODSFLQASVPPNNYLETTESSPECTVHLKTKGKICATKLSASSEDISER 116  
QY 931 LAGVSVGLPSS-----TTEOPKPAVQTKGRPSQCLNSSLPSLS--HAQLMFPAPSAFCSSA 170  
DB 117 LAGVSVGLPSS-----TTEOPKPAVQTKGRPSQCLNSSLPSLS--HAQLMFPAPSAFCSSA 170  
QY 991 PSVPAGTATVSKHRLQGFIPCRIPASPOTKRFSLOGRNCPENKSDKLSFVQSPR 1050  
DB 171 PSVP-----DISKRNQAFVPCIKIPASPOTKRFSLOGRNCPENKSDKLSFVQSPR 225  
QY 1051 PLPSSNHRPKPSRPTPGNTSKOGDPSKNSMTLDLNSSSKCDSPGCCSSNSNAVIPSDE 1110  
DB 226 PLPSSNHRPKPSRPTPGNTSKOGDPSKNSMTLDLNSSSKCDSPGCCSSNSNAVIPSDE 285  
QY 1111 TVFTPVBEKCRDLVNTLNSIEDLLEASMPSSDTVTYFKSEYAVLSPKAEKNDYTKDD 1170  
DB 286 TVFTPVBEKCRDLVNTLNSIEDLLEASMPSSDTVTYFKSEYAVLSPKAEKNDYTKDD 345  
QY 1171 VNNHOKCKEKMEAEFEALAIAMAMASODALPIYQLOVENGEDIIIIQODTPETLPGH 1230  
DB 346 VNNHOKCKEKMEAEFEALAIAMAMASODALPIYQLOVENGEDIIIIQODTPETLPGH 405  
QY 1231 TRAKOPYREDTBMKGOQIGLAFSSCYQAOQVGTGLMAVKQVTVRNTSSBOEYVEA 1290  
DB 406 TRAKOPYREDTBMKGOQIGLAFSSCYQAOQVGTGLMAVKQVTVRNTSSBOEYVEA 465  
QY 1291 LREIRIMASHLNHPNIIIRMLGATEKSNYMLFEMMAGSAVHLSTYGAFFKESVINYT 1350  
DB 466 LREIRIMASHLNHPNIIIRMLGATEKSNYMLFEMMAGSAVHLSTYGAFFKESVINYT 525  
QY 1351 EOLRGLSTYHENOIIHRDVGANLLIDSTGQRLRIADFGAARLASKGTGAGFQQL 1410  
DB 526 EOLRGLSTYHENOIIHRDVGANLLIDSTGQRLRIADFGAARLASKGTGAGFQQL 585  
QY 1411 GTIAFMAPEVLRGOOYGRSCDWMVSGCAIIEMACAKPNNAEKSHNLALIFKIASATTA 1470  
DB 586 GTIAFMAPEVLRGOOYGRSCDWMVSGCAIIEMACAKPNNAEKSHNLALIFKIASATTA 645

Oy 1471 PSLPSPGLSPGLRVALLKCELOPODRPPSRRELLKHPVFRITW 1512  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 646 PSLPSPGLSPGLRVAVKCELOPODRPPSRRELLKHPVFRITW 687  
 RESULT 3  
 S20117  
 protein kinase BCK1 (EC 2.7.1.-) - yeast (*Saccharomyces cerevisiae*)  
 N:Alternate names: protein J0906; protein kinase SLK1; protein kinase SFP31; protein YJL  
 C:Species: *Saccharomyces cerevisiae*  
 C:Date: 23-Apr-1993 #sequence, revision 23-Apr-1993 #text change 24-Sep-1999  
 A:Accession: S20117; S50285; S22285; S19061; J01432; S56872; S30794; J01118  
 R:Costigan, C.; Gehring, S.; Snyder, M.  
 M:Cell. Biol. 12, 1162-1178, 1992  
 A:Title: A synthetic lethal screen identifies SLK1, a novel protein kinase homolog implicated  
 A:Reference number: S20117; NCID:92186847; PMID:1545797  
 A:Accession: S20117  
 A:Molecule type: DNA  
 A:Residues: 1-1478 <COS>  
 A:Cross-references: EMBL:M84389  
 A:Experimental source: strain S288C  
 R:Miosga, T.; Boles, E.; Schaeff-Gerstenschlaeger, I.; Schmitt, S.; Zimmermann, F.K.  
 Yeast 10, 1481-1488, 1994  
 A:Title: Sequence and function analysis of a 9.74 kb fragment of *Saccharomyces cerevisiae*  
 A:Reference number: S50295; NCID:9516706; PMID:7871887  
 A:Accession: S50298  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1478 <MIO>  
 A:Cross-references: EMBL:X77923; NCID:9640004; PIDD:CAA54896.1; PID:9640009  
 R:Lee, K.S.; Levin, D.E.  
 Mol. Cell. Biol. 12, 172-182, 1992  
 A:Title: Dominant mutations in a gene encoding a putative protein kinase (BCK1) bypass t  
 A:Reference number: S22285; NCID:92107166; PMID:1729597  
 A:Accession: S22285  
 A:Molecule type: DNA  
 A:Residues: 1-58, 'I', 60-1478 <LEE>  
 A:Cross-references: EMBL:X60227  
 A:Experimental source: strain EG123  
 R:Lee, K.S.; Levin, D.E.  
 Submitted to the EMBL Data Library, June 1991  
 A:Description: An extragenic suppressor of mutations in the *S. cerevisiae* protein kinase  
 A:Reference number: S19061  
 A:Accession: S19061  
 A:Molecule type: DNA  
 A:Residues: 1-58, 'I', 60-263, 'P', 265-278, 'I', 280-702, 'S', 707-708, 'KP', 714, 'VITMTE', 715-79  
 A:Cross-references: EMBL:X60227; NCID:93414; PIDD:CAA42788.1; PID:93415  
 A:Experimental source: strain EG123  
 R:Title, K.; Araki, H.; Oshima, Y.  
 Gene 108, 139-144, 1991  
 A:Title: A new protein kinase, SFP31, modulating the SMP3 gene-product involved in plas  
 A:Reference number: J01432; NCID:92104496; PMID:1840547  
 A:Accession: J01432  
 A:Molecule type: DNA  
 A:Residues: 149-1478 <IRI>  
 A:Cross-references: EMBL:D10389; DDBJ:D90446  
 R:Miosga, T.; Schaeff-Gerstenschlaeger, I.; Baur, A.; Boles, E.; Chalwatzis, N.; Fournie  
 Submitted to the Protein Sequence Database, September 1995  
 A:Reference number: S56855  
 A:Accession: S56872  
 A:Molecule type: DNA  
 A:Residues: 1-1478 <MIW>  
 A:Cross-references: EMBL:Z49370; NCID:91008269; PIDD:CAA89389.1; PID:91008270; MIPS:YJL09  
 R:Usick, M.E.  
 Submitted to the EMBL Data Library, March 1992  
 A:Reference number: S27437  
 A:Accession: S30794  
 A:Molecule type: DNA  
 A:Residues: 602-959, 'R', 961, 'R', 963-1085, 'V', 1087, 'SLTIAHT', 1092-1094, 'RMD', 1101, 'TV', 11  
 A:Cross-references: EMBL:M88604; NCID:9172073; PIDD:AAA21179.1; PID:9172074  
 C:Genetics:  
 A:Gene: SGD:BCK1; SLK1; SFP31  
 A:Cross-references: SGD:S0003631; MIPS:YJL095W

A:Map position:10L

C:Function:  
A:Description: phosphotransferase; protein kinase; involved in cell proliferation  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom  
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protei  
F:1173-1440/Domain: protein kinase homology <KIN>  
F:1181-1189/Region: protein kinase ATP-binding motif

Query Match 7.9%; Score 619; DB 2; Length 1478;  
Best Local Similarity 21.0%; Pred. No. 1,4e-14;  
Matches 332; Conservative 232; Mismatches 552; Indels 466; Gaps 64;

DY 224 EMNHLAESPEEVAQASAPSKGR-----RSPSE--NSPSGRTVSESPPVKRR 273  
Dd : : : : : : : : : : : : : : : : : :  
Db KFGHDPSSVSATSRSSPRATSRKSIYDDIRSQFPLTPNSYSOFYES----- 74  
DY 274 VSPVFOSGRITPPRPARSPGCFSPYSPEETNRNRNKVMRAKLILQOIGNSPLIGDS 333  
Dd : : : : : : : : : : : : : : : : : :  
Db -TVLEGSFNMT-----TDHISAGTILE-----NFTSTNSSYK 107  
DY 334 PDNKRYVEFIGPONSICAR---GTFCIHLLRVFLVPLESDPMILW---RKT----- 379  
Dd : : : : : : : : : : : : : : : : : :  
Db 108 NDN-----GPSLSDSKKSGSNGSVNSLSPDKILLMSDPDRPDWMTHRTSMFKPHDF 161  
DY 380 -----LKNEVESLFQKYHSRRSSRIKADSRNTIQKFVR-MSNS 418  
Dd : : : : : : : : : : : : : : : : : :  
Db 162 PESWIPEFKKHQLGFGRFIKLIAYDNFAVYEKYLPTQKTASYTRFOOLIKTKMTKNVTNS 221  
DY 419 H-----TLSSSTSTSSSENSIKDEEOQCPICLGLMDESLVTCEDSC-----RNK 466  
Dd : : : : : : : : : : : : : : : : : :  
Db 222 HIROKSASKLKRSSSSSSISKLNKSKSQE-DISNSRSTESALSPKSGSPSTDEKNF 280  
DY 467 LHHHCMSIWAEECRNRREPLICPLCRSKWRHDEFSEHLSVPVSPSSLYRAAOQTVOOQ 526  
Dd : : : : : : : : : : : : : : : : : :  
Db 281 LH-----STSHHQTKKKSASLYLRSFILRGSSSNMASAPSNIKTL----STPAR 328  
DY 527 PLASRRNOESNFNIETHGYOOIPPAYKDIAEPMLIOVFEMLVGCFSFRNNVREMALAR 586  
Dd : : : : : : : : : : : : : : : : : :  
Db 329 P-----HSIIENSTLTWKASPSPASPSYPS-----IFRRH-----HK 360  
DY 587 LSHDVSGALLANGESTONSGSSSSSPSGCATGSS-----QTSISGDVVEACCS 637  
Dd : : : : : : : : : : : : : : : : : :  
Db 361 SSSSESSLNLSLFGSIGIEEAPT-K-PNQGHSLSENLAKGSKHYEYNVSSPKQS--- 416  
DY 638 VLNMWCAPPVKKVYAALKLTRAMLVYPCHSLAEIKILOQLPVVDTLIVKCADNSR 697  
Dd : : : : : : : : : : : : : : : : : :  
Db 417 --SLPTSDDKGNLM---NKKFRKSOIGVSPNTYAVYTISO-----ETPSLK---SNS 461  
DY 698 TSQLSISTFL-----LELCQGQAGELAVGREILKAGSIGIGVDVYLNCILGN 744  
Dd : : : : : : : : : : : : : : : : : :  
Db 462 TATLTVGADVANIPESSSPPIPTANRSLEVISTEDTPRISSGTASFKTYDCINPD 521  
DY 745 QT---ENNMOELLGRCLIDRLLEPAFEYYPHVISTDVSQA-----PV 787  
Dd : : : : : : : : : : : : : : : : : :  
Db 522 KTVPPVANN-QKSYXKNLLDQ-----KEYP-LKKTGLDSENKYILTVKDNVSEVPL 572  
DY 788 EIR-YKTLISLTFPLQSIDNSHMV-----GK 814  
Dd : : : : : : : : : : : : : : : : : :  
Db 573 NIKSAVALISRRESALTYLGINHKNVTFHMTDFDCCIGAIPDTDLLEFLKSLFNTSGK 632  
DY 815 LSRRITYLSARWVTTVPVHFESKLEMLSVSSSTHTFRMRRIAMAIADEVETAEAIO--LG 872  
Dd : : : : : : : : : : : : : : : : : :  
Db 633 IYIKQOMLLOOKPKRAPILTSENVPILKSVKSSKRSOSTSLIASSTDVSI.VTSSSDITS 692  
DY 873 VEDITLDGGODSFLQASVNNLTLETENSPP-----ECYVHLEKTGGLCAT--KL 920  
Dd : : : : : : : : : : : : : : : : : :  
Db 693 FDEHASGGGRRYPQ--TPSYYYDRVSNTPTEELINYMIKEIVLHEEENAPMPAVEKTPKL 750  
DY 921 SASSEDISERLASISVGGSSSTTTTTTTTEDPKPMVQCKGRPHOCINSS-----PLSH 975  
Dd : : : : : : : : : : : : : : : : : :  
Db 751 ELINDPKGSKL-----NIPTITNESKSSFQVLARKDGTEIDENRH 792  
DY 976 SOLMF--PALTPSSSTPYVAGTADYDSKRLDGFICRIPASAPOTQRKFSQFHRNC 1033

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Db 793 RESPTKPELA-PKRARPANTSPQRTLISTSTKONKPIRLVASTKISNS-----842
QY 1034 PENKSDKLSPTVGTQRPPLSSNIHRP-KSRPTPGNTSKQDPSKNSMTL-----D 1084
Db 843 -----KRSKPLRPOLLSSPIEASSSSPSDLSSTYTPASHVHLIPQYKAND 889
QY 1085 LNSSKCD-DSFCCSS-----NSSNAVPEDETFV---TP-----VEEKRL 1122
Db 890 VMRLTDDSTSTSPSLKKKKQVKNRSNSTVSTNSIFSPSPDLKGNKSRVVSSTSA 949
QY 1123 DVNTELNSTIEDLLEASMP-----SSDTVPFKSEVAV-----LSPEKAEN 1163
Db 950 DIFEE-----NDITPADAPMPDSDSDSSDDIINSKKKTAPETNNENKKDEKSDN 1004
QY 1164 DDTYKDVNHNOKCKEKE-----AEEELATATAMASQDA 1201
Db 1005 SSTHSDIETFDSTQDKMEKKMTFRSPPEVYVGNLEKFPFRALMDKPIETGIASPTSPKS 1064
QY 1202 L-----PIVQLOVE-----NGEDITITIOQDP-----1224
Db 1065 LPSLSPKNVASSRTEPSTSPRPVPPDSSVEFTQDGLNGKNKPLNOAKTEPKRTKRTITIA 1124
QY 1225 -----ETLPGH-----TKAKQPYREDEE-WLKGOQIGL 1252
Db 1125 HEASLARKNSVLIKRONTKMGTRMVEVTENHNVSTINKAKNSGKYEKFRAMKGMIGKG 1184
QY 1253 AESSCYQADVGTGLMAVQKQVTVYNTSDEQEV---VEALREETRMNSHLNHPITRM 1309
Db 1185 SGCAVYLCTNVTGEMMAVQVE-VPKYSQNSQALISTVEALRSEVSTLKDLHLNIYQY 1243
QY 1310 LGATCKSNVNFIEEMAGSVANHLISKGAFESVYINTBDLLGLSTLHENOIHRD 1369
Db 1244 LGEMNNNNITSLFEVAVAGSVGLRMGRFEPEDIKHLITTVYGLGLALSHKGLIHRD 1303
QY 1370 VGANLLIDSTGQRIRIADFGAARLASKGTGAGEFQGLGTITAFMAPEVLKGOO-YGR 1428
Db 1304 MMADNLLDQDG-ICKISDFGISRK--SKDIYNS-DIMMRGVFMAPAMVMTKOCYSA 1359
QY 1429 SCQVMSVCAIIEMACAPPMNAEKSNHLAIFKTASATTAPSDPSHLSPLGRVALR- 1487
Db 1360 KVDIMVLGIVLEMFAGKRPMS---NLEVAAMFKIGKSKAPPIEDTLPLISQIGRNF 1416
QY 1488 ---CLELOPQDPRPSRELLKHP 1506
Db 1417 LDACEFINPEKRPANELLISHP 1438

```

## RESULT 4

```

A48084
SPELL protein kinase homolog NPRI - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 19-Dec-1997
C:Accession: A48084
R:Banno, H.; Hirano, K.; Nakamura, T.; Irie, K.; Nomoto, S.; Matsumoto, K.; Machida, Y.
MOL. Cell. Biol. 13, 4745-4752, 1993
A:Title: NPRI, a tobacco gene that encodes a protein with a domain homologous to yeast E
A:Reference number: A48084; MUID:93330268; PMID:8336712
A:Accession: A48084
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-706 <BAN>
A:Experimental source: BY-2 cells
A:Note: sequence extracted from NCBI backbone (NCBIN:135697, NCBI:135698)
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP
F:94-358/Domain: protein kinase homology <KIN>
F:102-110/Region: protein kinase ATP-binding motif

```

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Query Match 7.6%; Score 595.5; DB 2; Length 706;
Best Local Similarity 42.0%; Pred. No. 4,6e-14;
Matches 121; Conservative 60; Mismatches 94; Indels 13; Gaps 6;

```

```

QY 1227 LPHGTRAKOP---YREDT---EMLKGOQIGLAFSSCYQADVGTGLMAVQKQVTVYRNT 1280
Db 74 LPSISKLELPKAKRKDTPPIRMRKGMKICGAFGRVYMMANNVDSGELLAIKEVSIAMG 133
QY 1281 SSQD--EEVEALREETRMNSHLNHPITIMLATGCKSNVNFIEEMAGSVANHLISKY 1338
Db 134 ASRRRAAHVRELEEEVNLKNSHPNIVYLTGARAGSLNITLFEVPGSSISLGLKRP 193
QY 1339 GARFESVINYTEQLLGLSTYLHENOIHRDVGANLLIDSTGQRIRIADFGAARLASK 1398
Db 194 GSFPESYIRMYTKQLLGLLEYLHKNGIMHRDIGNANLVDNKG-CIKLADFGASKVVEL 252
QY 1399 GTGAGFQGLGTITAFMAPEVLRGOQYGRSCDVMSVCAIIEMACAPPMNAEKSNHL 1458
Db 253 ATMTG--AKSMKGTPLYMAPEVILQTHSFSADISWVGCTIIEAMGKPPMS--QOYQEV 308
QY 1459 ALIFKTASATTAPSDPSHLSPLGRVALRCLDLOPQDPRPSRELLKHP 1506
Db 309 ALPLHIGTYSHPPIRPHLSAESKDFLLKCLQEPHLRHSASNLQHP 356

```

## RESULT 5

```

A96591
NPRI-related protein kinase 2 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C:Accession: A96591
R:Theologis, A.; Ecker, J.R.; Palm, C.T.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chen, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A96591
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-651 <STO>
A:Cross-references: GB:A8005173; NID:g9857521; PIDN:AAG00876.1; GSPDB:GN00141
C:Genetics:
A:Gene: T24C10.7
A:Map position: 1
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

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```

Query Match 7.6%; Score 591.5; DB 2; Length 651;
Best Local Similarity 43.3%; Pred. No. 5,8e-14;
Matches 119; Conservative 55; Mismatches 90; Indels 11; Gaps 5;

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QY 1234 KQPYREDTEMLKQOIGLAFSSCYQADVGTGLMAVQKQVTVYRNTSSQD--EEVEAL 1291
Db 63 KPIR---WRKQOLIGRAFQGVYVGMNIDSELLAVKQVLTSCAKSEKQIAHIOEL 118
QY 1292 REEIRMSHLNHPITIMLATGCKSNVNFIEEMAGSVANHLISKYGARFESVINYTE 1351
Db 119 EEEVKLKLKNSHPNIVYLTGAREDELNITLFEVPGSSISLLEKFAPEESVRYTNN 178
QY 1352 QLLRGSLYLHENOIHRDVGANLLIDSTGQRIRIADFGAARLASKGTGAGFQGLG 1411
Db 179 QLLRGSLYLHENOIHRDVGANLLIDSTGQRIRIADFGAARLASKGTGAGFQGLG 1411
QY 1412 TIFMAPEVLRGOQYGRSCDVMSVCAIIEMACAPPMNAEKSNHLAIFKTASATTAP 1471
Db 236 TIFMAPEVLRGOQYGRSCDVMSVCAIIEMACAPPMNAEKSNHLAIFKTASATTAP 1471
QY 1472 SIPSHLSPLGRVALRCLDLOPQDPRPSRELLKHP 1506
Db 294 PIPDNISSANDPFLKCLQEPHLRHSASNLQHP 358

```

RESULT 6  
 MAP kinase kinase kinase - yeast (*Kluyveromyces marxianus* var. *lactis*)  
 T30565  
 C:Species: *Kluyveromyces marxianus* var. *lactis*, *Candida sphaerica*  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
 C:Accession: T30565  
 R:Jacoby, J.D.; Kirchrath, L.; Gengenbacher, U.; Heinisch, J.J.  
 J. Mol. Biol. 288, 337-352, 1999  
 A:Title: Characterization of K1BCK1, encoding a MAP kinase kinase kinase of *Kluyveromyces*  
 A:Reference number: 220862; MID:99262846; PMID:10329146  
 A:Accession: T30565  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1338 <C>  
 A:Cross-references: EMBL:AJ005079; NID:g3021328; PIDN:CAA06336.1; PID:g3021329  
 C:Genetics:  
 A:Note: BCK1  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 7.1%; Score 552.5; DB 2; Length 1338;  
 Best Local Similarity 25.0%; Pred. No. 2.6e-12;  
 Matches 211; Conservative 149; Mismatches 338; Indels 147; Gaps 32;

QY 741 ILGNQESNMWQELGRLCLID-----RLLEFPAEFYHYSTDV-----SQAEVE 788  
 DB 535 VKSNASASNGESSDLTSDGSSHRRAVPQTPSHYDNGTSATFDWSPKDSVPE 594  
 QY 789 IRYKKLILTLFALQSDINSHWGLSRITLSSAMVTVPVFESK-LLEMLSVSSST 847  
 DB 595 IS-----DAHITLPKSRPLKLNSSVLT--HASEKSTFRITRIOTSDT 636  
 QY 848 HFTMRRLMALDEVEIAEAIQGVEDTLDGQDSFLQASVPNNYLETTENSPECTVH 907  
 DB 637 DIDFNKRRESPPYVALAPK-RKAPKPVNG--NPVTSGLSPAAKNVSESLESPK 693  
 QY 908 LEKTKGKL-----CATKLSA-----SSEDISESLAISVGPSSSTTTT 949  
 DB 694 LDRNGKTIYKNNKPRPPPLTTERSSRSVSSLSGQDINE--VKSPVOSTPASTOV 749  
 QY 950 EOPKP-----MVOTKGRPHSOCLNESP-----LSHHSOLFPALSTP-----SSSTPS 992  
 DB 750 MVRQPYGALETCLKPKSSADLSIRPMKSLKQFRSNNSLRNKYLSTSRQTLNTNSKPL 809  
 QY 993 VPACTATDVSKHRLQGITPCRPISAPQOTOKRFSLQFHRNCPENKDSKISP-----VFT 1047  
 DB 810 VTSSTATDIDENDISE-----ADAPELSDSDSYASASDEITWS 848  
 QY 1048 QSRPLPSNTHRPKSPRTGNTSKQDPSKNSMTLDLNSSKCDDEFGCSNSN----- 1103  
 DB 849 RDRKSISNDV--PEFSNTED-----TIDLVGDTTQVSVGATEGSDTPKRM 893  
 QY 1104 AVIPSDVETFPVEEKRCLDVNTLEANSIEDLEASMPSPDTVTYFKSEVAVLSPEKAE 1163  
 DB 894 ALRSPPVVYQNL-EKFPPLADLD-NPILBGLTPPPSPNADSPSPRGPFKSLKTSEQ 951  
 QY 1164 DDTYKDDVNNQK---CKEKMEAEEDBALAIAMASASQDALPIVQ-LQVEN-----GE 1214  
 DB 952 QPAFLSSRGSSSOFITPVKSLKPKRKTKTIRI-IAQASSEARKNEVSEQKLQKTKMMGT 1010  
 QY 1215 DIIIIQODTEPTLPGHKKAKQPYREDTEBMLKGOIIGLQASFCSCQAOQVCGITLMAKQV 1274  
 DB 1011 KVEITDKRTISINKSNRSKEYE-FAMIKGELITGKSGFCAVYLAIAVNTTGEMLAYQV 1069  
 QY 1275 TVYVNTSEOE---EVEVALREEIFRMAHSHLNHPNIIIRMLGATCEKSNYNIETEMAGSV 1331  
 DB 1070 T-VPEFSODESALSNWEALKSEVSTLKDNLNHNVIYQILGEERKNQISLPLEVYAGGSV 1128  
 QY 1332 AHLISKYGAERESVAVITTEQLGLSYLHENOIIIRDVKCANLIDSTGRLRIADFGA 1391  
 DB 1129 GSTLRMGREFPDOLIRHLTKQVLEGLAVIHSKGIILHRDKMADNLLDNDVQ-CRISDGI 1187  
 QY 1392 AARLASCTGAGFEQGLGIAFMARVPL-RGOQYGRSCHVSVGCAIIMACAPPMN 1450

DB 1188 SRKSNNTYSNS---DMTRGTVFMWAPBMDVTANGYSKAKVDIWSLGCYVLEMPAGKRPWS 1244  
 QY 1451 AEKSNHNLALIFKIASATTPASIPSH---LSPGLRDVALRCLEQDPDRPPRELKHP 1506  
 DB 1245 ---NFEVVAANFQIGKSTAPPIPDFTKDYLSPPAGQSLDQCFEIDPEMRFTASIVGHP 1301  
 QY 1507 VERFTT 1511  
 DB 1302 FCKTS 1306

RESULT 7  
 A39723  
 protein kinase byr2 (EC 2.7.1.1) - fission yeast (*Schizosaccharomyces pombe*)  
 N:Alternate names: protein kinase ste8  
 C:Species: *Schizosaccharomyces pombe*  
 C:Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 15-Sep-2000  
 C:Accession: A39723; S30094; T39860; T40139  
 R:Wang, Y.; Xu, H.P.; Riggs, M.; Rodgers, L.; Wiggler, M.  
 Mol. Cell. Biol. 11, 3554-3563, 1991  
 A:Title: byr2, a *Schizosaccharomyces pombe* gene encoding a protein kinase capable of  
 A:Reference number: A39723; MID:91260705; PMID:2046669  
 A:Accession: A39723

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-659 <MO>  
 A:Cross-references: GB:M74293; NID:g173352; PIDN:AAA35289.1; PID:g173353  
 R:Styrksgottliir, U.; Egel, R.; Nielsen, O.  
 Mol. Gen. Genet. 235, 122-130, 1992  
 A:Title: Functional conservation between *Schizosaccharomyces pombe* ste8 and *Saccharom*  
 A:Reference number: S30094; MID:93062799; PMID:1435723  
 A:Accession: S30094  
 A:Molecule type: DNA  
 A:Residues: 1-659 <STY>  
 A:Cross-references: EMBL:X68851; NID:g5106; PIDN:CAA48731.1; PID:g5107  
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.  
 submitted to the EMBL Data Library, August 1997  
 A:Reference number: Z21886  
 A:Accession: T39860

A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-659 <MO>  
 A:Cross-references: EMBL:Z98270; PIDN:CAB10981.1; GSPDB:GN00067; SPDB:SPBC1D7.05C  
 A:Experimental source: strain 972h; cosmid c1d7  
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.  
 submitted to the EMBL Data Library, June 1997  
 A:Reference number: Z21907  
 A:Accession: T40139

A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 298-659 <MO2>  
 A:Cross-references: EMBL:Z97211; PIDN:CAB10150.1; GSPDB:GN00067; SPDB:SPBC2F12.01  
 A:Experimental source: strain 972h; cosmid c2F12  
 C:Genetics:  
 A:Gene: byr2; ste8  
 A:Map position: 2  
 C:Superfamily: protein kinase byr2; protein kinase homology; SAM homology  
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
 F:1-66/Domain: SAM homology <SAM>  
 F:392-658/Domain: protein kinase homology <KIN>  
 F:400-408/Region: protein kinase ATP-binding motif

Query Match 6.9%; Score 543.5; DB 1; Length 659;  
 Best Local Similarity 26.2%; Pred. No. 2.7e-13;  
 Matches 181; Conservative 115; Mismatches 259; Indels 137; Gaps 27;

QY 871 LGVEDTLDGQDSFLQASVPNNYLETTENSPP-----EC---TVNLEKTKG---KGLCAT 918  
 DB 46 LGINTATAGKQ--FLK---QRDYLR--EFPPCILRFYACNGQTRAVQSGRDYQKTLAIA 98  
 QY 919 KLSASSEDISRLASISVGPSSSTTTTTEQPRPMVOTGRHRSQCLNSPLSHSQ 978  
 DB 99 LKRFSLDASKFIVCV---SSSSRIKLITEERKQI-----CFNSSSPERDLI 144

[illegible]

Db 26 KLGFASEDSSRCRSKRRRRDEIVSEKGAISRLPSRSRSPSTRVRSRQGSFAERSRPAAPL 85  
Y 952 PKPMVQTGRPHSQCLNS-----PLSHSQLMFPLSLTPSSSTPSVPACTATD----- 1000  
Db 86 PAPIY-----RPVYISTDGMNGSORPGDANLKPRLMPLPKFHGAT-SIPDNTGAEPDFA 140  
Y 1001 ---VAKHRLGGRIP-----CRIPASAPQGRKFSLQFHNCENKNDSDSLSPVF 1046  
Db 141 TASVSGSGSVGDIPEDSILSLPLASCSCEGNGNRPVNISSRDSMSHN---KNSAEKFKVP 197  
Y 1047 TQSRPLPSSNIHRP-----KPSRP----TPGNTSKOG- 1074  
Db 198 NKNRILSLSPRRRPGTHVKNLQIPQRDLVLCAPADSLSSPSRSPMSRFPIDQVSNHGL 257  
Y 1075 DPKSKMTLIDNSSKCGDSSRGCSNSSNNAVLPD--ETVTPPYREKRLDYNELNSI 1132  
Db 258 LISKYIDVSLGSGQC--SPSGSYNSGNSISGGMATQLEWP-QSRC---SPCSFVP 311  
Y 1133 EDLEASMPSSDTTYTFKSEVAVLSP--KAENDTYKDDVNHNQKCEKMEAEFEAL 1189  
Db 312 SPRMTSPQSSRIQ---SGAVTPLHPRAGSGTSGPTRRLDNNRQSHR----- 357  
Y 1190 AIAAMASQDALPVLPOLQYENEDITIIIOODIPETILPGHTA-----KQPIRED--- 1240  
Db 358 -----LPLRP-----LLISNTPCFS-PTYSAATSPVSPSPAAEATV 394  
Y 1241 ---FWMLGGQOIGGAFSSCYOAOQVGTGTLMAYQVYVYRNTSSEGEVEALREETRM 1297  
Db 395 SPGSMKKKGRLLMGSEFGHYLGFNISEGEMCAKEVILCSDDPRSRS--AOQLGQELSV 453  
Y 1298 MSHLNHPNIIIRMLGATCEKSNLYNFIEEMAGGSVAHLLSKYGAFEKSVYINTYEQLLRGL 1357  
Db 454 LSRLEHONTIVQYSGSEFVDDKLTYILEVYSGSGSIYKLLQEGQFENAIRVYTOOILSGL 513  
Y 1358 SYLHENQIHHDVGNANLIDSTGQRILRIPDGAARLASKGTGGEQGLGIANMA 1417  
Db 514 AYLAHAKTAVHDIDIKANLILVDPHG-RVKVADPGMAKKHTTAQ-SGLSPFK---GSPYMA 567  
Y 1418 PEVLNGOQYGR-SCDVMSVGCATIEMACAPPMNAEKSHNLALFLKASATTAAPISPH 1476  
Db 568 PEVINSNGSNMLAVDIMSIGCTVLEMATTKPWS--QYEGVPMKFKIGNSKELPDIDPH 624  
Y 1477 LSPGLRDVALKCLDELQODRPPRSRLKHVYFR 1509  
Db 625 LSECKDFVRCCLQNRPNRPTAQLLDHAFVR 657

RESULT 9  
S51380  
protein kinase STE11 (EC 2.7.1.-) - yeast (*Saccharomyces cerevisiae*)  
N/Alternate names: protein L8039.10; protein YLR362w  
C/Species: *Saccharomyces cerevisiae*  
C/Date: 23-Feb-1995 #sequence-revision 11-Aug-1995 #text-change 21-Jul-2000  
C/Accession: S51380; A36456  
R/Dn: Z.  
submitted to the EMBL Data Library, December 1994  
A/Description: The sequence of *S. cerevisiae* cosmid 8039.  
A/Reference number: S51377  
A/Accession: S51380  
A/Molecule type: DNA  
A/Residues: 1-738 <DUZ>  
A/Cross-references: EMBL:U19103; NID:q609404; PIDN:AAB67571.1; PID:q609414; GSPDB:GNO  
R/Rhodes, N.; Connell, L.; Ertede, B.  
Genes Dev. 4, 1862-1874, 1990  
A/Title: STE11 is a protein kinase required for cell-type-specific transcription and  
A/Reference number: A36456; MUID:91115076; PMID:2276621  
A/Accession: A36456  
A/Molecule type: DNA  
A/Residues: 1-717 <RHO>  
A/Cross-references: GB:X53431  
A/Genetics:  
A/Gene: SGD:STE11; MIPS:YLR362w

A:Cross-references: SGD:S0004354; MIPS:YLR362w  
 A:Map position: 12R  
 C:Superfamily: 12R  
 C:Keywords: ATP; phosphotransferase; protein kinase  
 F:38-104/Domain: SAM homology <SAM>  
 F:442-733/Domain: protein kinase homology <KIN>  
 F:442-450/Region: protein kinase ATP-binding motif

Query Match 6.8%; Score 535; DB 1; Length 738;  
 Best Local Similarity 25.2%; Pred. No. 5.9e-12;  
 Matches 205; Conservative 117; Mismatches 215; Indels 276; Gaps 35;

QY 781 VSOAPEVPIRKLLSLTFLP-----QSIDNSHMKGL-----SRRIYLSA----- 824  
 DB 108 IEQVNRKKNLMKESVSLSTATLSMNSSELIPKHCVFILINDGSAKKVAVNCCFNADSIK 167  
 QY 825 RMVTVPHVFESKLEMLSVSSSTHTFM-----RRRLMAIDVEVLAIAIQGV 873  
 DB 168 RLIRLPH-----ELLATNSNGEYTKAVDYDFVLDYTKNVLHLTYDELVTICH--A 219  
 QY 874 EDTLDGODSFLQAVPNVYLETTESSPECTVHLEK---TGKICATKLSSASEDISER 930  
 DB 220 NDVRE-----KNRLIFVSKDQPS-----DKAISTSKUYLTLSALSG----- 258  
 QY 931 LASISVGPSSSTTTTTEOPKPMVQTKGRPHS-----QCLNSSLPLS 973  
 DB 259 -----VPSRSSNL-----LAONKKGISHNNAEGLKIDNTEKDIRIQIFNQRP-- 300  
 QY 974 HHSQMLPPLSTPSSSPVPAGTATDVKSHRLOGFICRIPASPOQRKFSLOFHNC 1033  
 DB 301 -----PSEFISTNLATGTFPHITDMKRLQ-----KTMRE----- 327  
 QY 1034 PENKSDKLSFVFTQSRPL--PSSNIHRKPSRPTPGNTSKQGPSPKNSMTLDLNSSKC 1091  
 DB 328 -SFRHSARLS--IAQRRLSAESNNI-----GD----- 352  
 QY 1092 DDSFGCSSNSNAVIPSDEYFTVEEKCRLDVTELNSSIEDLLEASMPSSDTTVTKS 1151  
 DB 353 -----ILKHSNAV--DMALLOGLDQ-----TRLSKL-----DPT----- 381  
 QY 1152 EVAVLSPEKAAANDPYKDVVHNOCKCKEKEEPEEALATAMASASODALPIYQLOVE 1211  
 DB 382 KIPKLAHKRPDNDALIS-----NOLELIVSEGE-----DHDF----- 417  
 QY 1212 NGEDIILIIQODPTPELPGHTKAKOPYREDTEMLGQOIGLGFSSCYQADVGTGLMAV 1271  
 DB 418 -GEQSDIV-----SLP--TKIATP-----KNMLKAGACIGSGSPGVYLGMAHNGELMAV 464  
 QY 1272 KQTVTVRNT-----SSQOE-----VEALRE 1293  
 DB 465 KOVEIKNNNIGVPTDNKNQANSDENNEQEQOEKIEDYGAVSHPTQNINHRKNVDALQH 524  
 QY 1294 EIRMSHLNHPNIIIRMGATCEKSNYNLFITEMAGGSVAHLISYGAKESEVINYTQOL 1353  
 DB 525 EMNLKLEHHEINIVTYYGASQEGGGLNTELEYPGGSVSMNNNGPEESLITNFTQOI 584  
 QY 1354 LRGLSYLHENOIIHRDVKAGMLIDSTGQRLIADFGAARLASKGTAGFEOGLCTI 1413  
 DB 585 LIGVAYLHKNNIHRDILKGANILIDING-CVKITDFGSKLSPLUNKONK-RASLOSIV 642  
 QY 1414 AFMAPEVLRGQOYGRSCDVSVGCAIITEMACAPPMNAEKSHNLALFKIATATPASI 1473  
 DB 643 FMSPEVAVKQATATYAKADIMSTGCIVIEFMFGKHPF--PDFSQOALFKIGTNTT--PEI 698  
 QY 1474 PSHLSPGLRDVALRCLQLQODRPPRELKHP 1506  
 DB 699 PSMAISEGKNFLKAFELDIYRPSALELQHP 731

RESULT 10  
 G96575  
 probable MKK kinase MAP3Ka, 84794-81452 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: G96575  
 R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar,  
 ansen, N.F.; Hughes, B.; Hutzar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitli, R.; Marzia  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: G96575  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-608 <STO>  
 A:Cross-references: GB:AE005173; NID:910645340; PIDN:AA621460.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: F22G10.18  
 A:Map position: 1

Query Match 6.8%; Score 531.5; DB 2; Length 608;  
 Best Local Similarity 27.3%; Pred. No. 6.5e-12;  
 Matches 145; Conservative 91; Mismatches 179; Indels 117; Gaps 17;

QY 1031 RNCPEKNDKLSPEVFTQSRPLPSSNIHRKPSRPTPGNTSKQGPSPKNSMTLDLNSSK 1090  
 DB 8 KSC-KNKK-DNHRGILISTDRDKSSAVVDDPLTTRGCT-----PR 47  
 QY 1091 CDDSEFGCSSNSNAVIPSDET-----VFEPV--EKCRLDVTELNSSIEDL--- 1135  
 DB 48 CSREFAGASSAFSG-FDSDSTFEKKCHPLRPLLSVSIHQDHVAGSGISVSVSS 106  
 QY 1136 -----LEASMPSSDTTVTFKSEVAVLSPEKAAANDPYKDVVHNOCKCKEKEEPEE 1187  
 DB 107 GSADDQSLVASRGRD--VFENVAAPRSPERSV----- 139  
 QY 1188 ALATIMASASODALPIYQLOVENGEDITIIIOOT-----PETLPGH 1230  
 DB 140 -----PRAATITTPPTSPRIQRLSG--VSIESTGKNDGRSSSECHPLRPTPTPTS 191  
 QY 1231 TKAKOPYRED-----TEMLGQOIGLGFSSCYQADVGTGLMAVQTVTVRNT 1280  
 DB 192 PSAYGSRIGGGEYETSPSGFTWKKKFLGSGTFCQVYLGFNSEKGMKALKEVVIDD 251  
 QY 1281 SSEQEVEVVALREIRMSHLNHPNIIIRMGATCEKSNYNLFITEMAGGSVAHLISYGA 1340  
 DB 252 QT-SKECKLOLNOEINLNOIHPNIVGYGSELSEETLSVLEYVSGSIHKILKLDYGS 310  
 QY 1341 FKESVIVVYTBOLLRLGLSYLHENOIIHRDVKGANLLIDSTGQRLIADFGAARLASGCT 1400  
 DB 311 FTEPIQNTTROIILGLVYLHGRNTVHRDVKGANLVDPNGE--IKLAPFGMAKHVTAYST 369  
 QY 1401 GAGEFOGOLGTIAMEAEVLRGQO-YGRSCDVSVGCAIITEMACAPPMNAEKSHNLA 1459  
 DB 370 -----MLSEKSPYMAAEVAVWSQNGYTHAVDWSLGTILEMAISKRPWS---QFEVVA 421  
 QY 1460 LIFKIASATTAPISPSHLSPLGRDVALRCLQODRPPRELKHPVFRRT 1511  
 DB 422 AIFKIGNSKDPPEIPDHLSDNAKNFIRCLQRPNPTVPRASOLEHPEPLRNT 473

RESULT 11  
 T38073  
 serine/threonine-protein kinase mkl1 - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
 C:Accession: T38073  
 R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
 submitted to the EMBL data library, April 1996  
 A:Reference number: Z21767  
 A:Accession: T38073

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1116 <CON>

A:Cross-References: EMBL:270690; PIDN:CAA94620.1; GSPDB:GN00066; SPDB:SPAC1F3.02C

A:Experimental source: strain 972h; cosmid c1f3

C:Genetics:

A:Gene: pmk1; SPDB:SPAC1F3.02C

A:Map position: 1

Query Match

Best Local Similarity 25.1%; Score 517.5; DB 2; Length 1116;

Matches 185; Conservative 113; Mismatches 287; Indels 153; Gaps 25;

```

859 INDEVEIAEIQGVEDTLDGQDSFLQASVPNNYLETENSSPECTVHLE-----909
424 LNSDFEITTA--GPNLSLSGHQ-----PDNKYYKGFSSAPNLAVELSRRRGPF 472
910 ---KTGKGLCATKLSASSEISERL-----ASISVSPSSSTTTT 946
473 EKIRGAKEGAKTILDATEQSEKKNFTYCRPHKVTTLKMPLNSGSSAPQSPSSNTSASV 532
947 TT-----TEQPKPVQTKGRPHSQCINSSPLSHNSQLMFPALSTPSSSTSPVAGTATD 1000
533 LFNFAVHNDPPRPPTETSSLRKKNLTTRRPSIRHAR-----SSPIDTG-HNE 580
1001 VSKHRLQGITPCRIIPASQOTQKFSLOF-----HNCPENKSDKLSPVFTQSRP---- 1051
581 ASKFSHTSFDP--KASSKSNSLKESEVALSEIPFEDAPRLDESJLSDGFMAIQPKOSS 638
1052 --LPSSNHRPKRPRPTPGNTSKQDPSKNSMTLDNNSSK-----C-DDSFCSSNSN 1103
639 SQVPRKNHNIQSKLSI--NTEAATDLKANEL-----SSKTPRYCRGDDRSISLPLST 691
1104 AVIPSEVFTFVEEKCRLDVNTLNSJEDLE-----ASMPSSD 1144
692 RLKSKHIRESPSSKVINSGNMEVRPSADLXEDYDFRPYDLDKVLVVDQSRMVSF 751
1145 TTYTFR---SEVAVLSPEKAENDTYKDDVNNHQCKEKEAEERELATAMMASQDA 1201
752 SKVSTPKKSVALLAREASE---ARKETRNHARRNKSGLNLRSSTKLM-----798
1202 LPTPOLQVENGEDIIIIODPPELTPGHTKAKOPYREDTEMLKGOQIGLGAFFSCYQAQ 1261
799 -----GSRIVELKPDITITSGSVSQNAIFK---WAKGELIGNGTIGKPYFLAM 843
1262 DVGCTGLAAVKQVTVYRNTSSF---OEVEVALREERIMSHLNHPNITRMGATCEKS 1317
844 NNTGELIYAVKQVEIPQTINGRHDQLRKDIVDSINAEISMADLDLNIYQIGFEKTER 903
1318 NYNLFTFEMWAGSVAHLLKYGAFKESVYINVTEDLLRGISYVHENQIIRDOVKANLLI 1377
904 DISIFLEYSGSGISGRCLNRYGFEQQLVREVSROVLAYGLSYHSGIILHRDKADNLLI 963
1378 DSTGRLRIADGAAARLASKGTGAGEFOGLGITAFAPEVLRG--OQYGRSCDWMVY 1435
964 DEDGV--CKISDPSIKSH--SDNYDNDANLMSQGSIFWMAPEVIHNDHGYSKAVDWSL 1020
1436 GCATITMACAKPPWNAEKSNHLALIFKTASATTAPSIDSHL---SPGLRDVALRCLEL 1491
1021 GCVVLEMLGRRPWSYDE--AIQAMFKLGTEKKAPRIPSELVSQVSPKAIQFLNACFTY 1077
1492 OPODRPSRELLKHVYR 1509
1078 MADVRFPTAEELLNHPMK 1095
```

RESULT 12

T03022

MAP kinase kinase kinase - human

C:Species: Homo sapiens (man)

C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 05-Nov-1999

C:Accession: T03022

R:Takekawa, M.; Posas, F.; Salto, H.

submitted to the EMBL Data Library, May 1997

A:Description: A human homolog of the yeast Sak2/Sak22 MAP kinase kinase kinase, MTK1

A:Reference number: Z14824

A:Accession: T03022

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1607 <TA>

A:Cross-References: EMBL:AF002715; NID:92352276; PIDN:AAB68804.1; PID:92352277

C:Genetics:

A:Note: MTK1

Query Match

Best Local Similarity 19.7%; Score 502.5; DB 2; Length 1607;

Matches 288; Conservative 239; Mismatches 574; Indels 363; Gaps 59;

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169 TLKGLHMDRPREPMIREKIKATCPAMKHEML---ERRNRR-----208
370 SLQALQKDYKRYAKAQQDQVQALCL-----MLNITKDLNQRLRMGYLGIKNLSDIG 423
209 GPVYVAPRIPYKGDSEMNHLAESPPEVQASAPASKGRSPGNSPGRTVKSESPG 268
424 WPFELIPSPSPKGNBEYEGDDTEGLKELSS-----TDESEBQ 465
269 VRKRYSPVPFQSGRTTPRRASPDPGFSPYSPETNRNRYKWRARLYLLOQIGNSFL 328
466 ISDPVY-----PETRPIDNSFDIQSDCISK-----LERLESEBDS 503
329 IGDSPDNKYRVFIPGONSCARGTFCIHLFPLMVLVFOLEPSPDPMLRKTLKNFVESL 388
504 LGMGAD-----WTEAG-FSRKLTITYPFV-----DKALQMKLRKL 542
389 FQKYHS-----RKSRIKAPSRNTIQFVRSMSNSHTLSSSSSTSSSE--NSIKDE 438
543 ILRLKLMGSLQARIALYVKNDRPFESEFPDPMGSDVQLSRTPPSEKCSAVME 602
439 EEQMCIILLGMD---EESLVCEGDCGNKTH--HHCSTIAECCRNRREPLQPL-- 490
603 E-----LKANDLPSEFAFLVL---CVLNLVYHECLKLEQ--RPAGEPSLSTIQ 650
491 ---CRSKWRS-----HDFYSHELSPVDSPPSSLRAAQOQTVOOQPLAGSRNOESNF 539
651 LVRECKEVLKGLMKQYQFMQVLEDEK-----DCNI 667
540 NLTHYGTQIIPRYKDLAEWIOV---GMLVCLFSRRKN-----VR--EMAL 564
688 DAFEDLHKMLMYFPYMRSMIOMLOOLPQASHSLNKLLEEMENFTKEITHYIRGSEAQ 747
585 RRLSHVSGALLANGESTGNSGSSGSGATGSSGTSISGQVVEACSVLSMWCA 644
748 GKLFCDIAGMLKSTGSELEFGIQESCAEFWTSADDSASDEITRSVTE-----ISRLAK 802
645 DPVYKVVVAALKTLRAMLVYTPCHSLAERIKILQRLQPVVDI---LVKCADANRSTSQ 700
803 ELFEHRENRASKALGPAKMLRKDLAEFRLSAPVRDLDVLKSKQYKVOIPLGENIQ 862
701 LSLSTLLEICKGQAGELANGREILKAGSIGIGVD-----YVLNCLIGNOTES 748
863 MFVPDPL---AEKSIILQILNAAA---GKDCSKSDVDLIDAYLLTLTKHGGRARD 912
749 N-----NMQELGRLLDLRLLLEPPAEFYPHIVSRDVSQAEEVEYTRYKKLSLFLAQ 803
913 SEDSKGTWEHQ-----PVKVPQVEYDILRSKQVD-----NLLLVNQ 951
804 SIDNSHWGKLSRRIYLSARWTVV-----PAVFSKLEMLSVSSSTHTPRARRL 856
952 S---AHLTI---QRKAFQGSIEGIMTLCOEQTSQVIAKALQQLK-----991
857 MAIADVEITAELQGVEDTLDGQDSFLQASVPNNYLETENSSPECTVHLEKGT---- 912
992 ---NDALTELCNRISNAI--DRVDMFTSEFDAEVESESYTLQOYRREAMIQGVNFGFEYH 1047
913 KGICATKLASSSDISERLASSISVGPSSSTTTTTTTEQPKPVVQTKGRPHSQCLNSPFL 972
```



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Db 1048 KEYVRLMSGEFRKIDKXYSFARKMANYLTGCESGRTRRPMATOGPFPLAIEPAFI 1107
Qy 973 SHHSQMLPFPALSTPSSSPSPAGTATDVSKHLOGFICRIPASAPOTQRKESLOFHRN 1032
Db 1108 SALPEDDFLSIQALMNEICGHVIG-----KPH-----SPVT--GLYLAIHKN 1147
Qy 1033 CPENKSDLSIPVFTQSRPL-----PSSNIHRKP-----SRPFGTSMKQGDPSKN 1079
Db 1148 SP-----RPKPVNPRCHSDPPNPHLIIPFGFSTRSPQARSHGSPAAA 1192
Qy 1080 SMTLDLNSSKCDSPGSSSNNAVIPSDETVFTPEEKCRLDVMTLNSIEDLEAS 1139
Db 1193 AAAAAVAASRSPSG-----DSVLPKS-----ISSADHTGSS 1227
Qy 1140 MPSSDTFTVFKSEVAV-----LSPKAEENDTYK--DDVNHNOCKE--KMAEEREAAL 1189
Db 1228 VPENDRLASIAELAQRSLSRHSSPTEERDEPAYPRKDSGSTRRSEWELRTLISQKDTA 1287
Qy 1190 AIAAMASASODALPIYPOLQVENGEDIIITQO--DTPETLPG--HFKAKOPYREDETWLK 1245
Db 1288 SKLPLEALQKSVRLFEEKRYREMRKRNIIQVCDTPKSYDNVMHGLR--KVTEFMQR 1344
Qy 1246 GOOIGLGAFFSCYQADVGTGLMAVKQVTVYVNTSSEGEVEAEALREIRMMSHLNHPN 1305
Db 1345 GKRTGGQYGYKTYTCTISVDTGELMAKKEIRFQPN----DHKTIKETRADELKITEGIRKHPN 1400
Qy 1306 IIRMLGATCEKSNYNIETEMAGGSVAHLISKYAFKESVAVIYTRQLRGLSYLHENOI 1365
Db 1401 LVYEFVEVLHREEMVIFMEYCEDEGTLEE--VSRLG--LQEHVIRLYSKQITAINVLEHGI 1458
Qy 1366 IHRDVGANLIDSTGQRRLADFGAARLASG--TGAGFQQLGTLAFMAPEVL--- 1421
Db 1459 VHHDDINGANIFLTSSG-LKLGDGCGSVKLNNAQRTMPGCV--NSTLGTAAVMAPEVITRA 1516
Qy 1422 RGOQYGRSCDVMSVGCATIEEMACAKPPMNAEKSHNLALFKIASATTAPISFHSPLG 1481
Db 1517 KEGHGRADINWLGCVIEMVYTGKRPWHYEH--NFQIMYKGMG--HKRPPIERLSPEG 1573
Qy 1482 RDVALRCLQLQDPPRPRELLKH 1505
Db 1574 KDFLSHCLSDPKRMWTASQLDHD 1597

RESULT 13
H66221
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H66221
R:Phelodis, A.; Ecker, J.R.; Palm, C.D.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chlin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltl, R.; Marzalli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakao, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A66141; MUID:21016719; PMID:11130712
A:Accession: H66221
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-652 <STO>
A:Cross-references: GB:AE005172; NID:g2142692; PIDN:AAB70419.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 6.2%; Score 484; DB 2; Length 652;
Best Local Similarity 37.3%; Pred. No. 3.1e-10;
Matches 113; Conservative 50; Mismatches 90; Indels 50; Gaps 10;
Qy 1228 PGHTAKOPYREDETWLKGOQIGLGAFFSCYQADVGTGLMAVKQVTVYVNTSSEGEV 1287

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Db 57 PANTVDMAF---PLSMRKGOLIGRAGFYMGNNLDGELAAKQVLAANFAS--KEK 111
Qy 1288 VEALREIRMMSHLNHNII-----RMGA-----TEKSN-----YNFETMMA 1327
Db 112 TQLEEEVVKLLKNSHNIVYVNCWYCLLNAAGFNFTSLCYLSNVVEDDTNLILEFVP 171
Qy 1328 GGSVAHLISKYGAFFKESVAVIYTRQLRGLSYLHENOIHRDVGANLIDSTGQRRLA 1387
Db 172 GGSISLLEKFGPPESVRYTRQLLGLLEYLNHNAIMHRDIGANILVDNNG--CIKLA 230
Qy 1388 DFGAANLASKGAGFQQLGTLAFMAPEVL--RGQOYG----- 1427
Db 231 DFGASKQVALALATWTG--AKSMGTPYMAPEVILQGHSPGDLCPILFISHKPAIVL 288
Qy 1428 RSCDVMSVGCATIEEMACAKPPMNAEKSHNLALFKIASATTAPISFHSPLGRVALR 1487
Db 289 SSADINWSGCVIEMVYTGKAPMS--QQYKEVAALFFGTTKSNRPIDPTLSSDAKDFLK 346
Qy 1488 CLE 1490
Db 347 CLQ 349

RESULT 14
T51625
MAPK alpha protein kinase (EC 2.7.1.-) [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 08-Sep-2000
C:Accession: T51625
R:Jouanin, S.; Hamal, A.; Leprieux, A.S.; Tregear, J.W.; Kreis, M.; Henry, Y.
Gene 229, 171-81, 1999
A:Title: Characterisation of novel plant genes encoding MEKK/STK1 and Raf-related pr
A:Reference number: 224447; MUID:9916996; PMID:10095117
A:Accession: T51625
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-582 <JOU>
A:Cross-references: EMBL:AJ010090; PIDN:CAA08994.1
C:Genetics:
A:Gene: MAP3K alpha
C:Keywords: phosphotransferase

Query Match 6.2%; Score 483; DB 2; Length 582;
Best Local Similarity 25.9%; Pred. No. 3e-10;
Matches 138; Conservative 84; Mismatches 166; Indels 144; Gaps 17;
Qy 1031 RNCPEKSDKLSIPVFTQSRPLPSSNIHRKPRSPRTGNTSKQGDPSKNSMTLDLNSSSK 1090
Db 8 KSC-KNRD-DNHRGILSTDRDIKSSAVYDP-PLTPRGGT-----PR 46
Qy 1091 CDDSPGSSSNNAVIPSDET-----VFTPV--EEKCRLDVNTLNSSTEDL---PR 1135
Db 47 CSREFAGASSAFSG-FPSDSTEEKGHPRLPRLSPVSIHHQDHYSGSTSVSYSSSS 105
Qy 1136 -----LEASMPSSDTFTVFKSEVAVLSPKAEENDTYKDDVNHNOCKEKEAEDEE 1187
Db 106 GSADPQQLVAASRGD--VKFNVAAPRSPERSV----- 138
Qy 1188 AIAAMASASODALPIYPOLQVENGEDIIITQODT-----PETLPGH 1230
Db 139 -----PKAATITTRPSPHQRLSG--VVSLESSTRNDGRSSSECHLPREPPTS 190
Qy 1231 TKAKOPYREDE-----TEMLKGOQIGLGAFFSCYQADVGTGLMAVKQVTVYVNT 1280
Db 191 PSAVHGRIGGVEYTSFGSGSTWKKGFLSGTGGVYILGFNSKGMCAIKYKVIYSD 250
Qy 1281 SSQEEVEVEALREIRMMSHLNHNIIIRMLGATCEKSNYNIETEMAGGSVAHLISKYGA 1340
Db 251 QT--SKELQKQINDINLNDLCHPNIVQYGGSELSEFTLSVLEYVAGGSIHKLKDYGS 309
Qy 1341 FKESVAVIYTRQLRGLSYLHENOIHRDVGANLIDSTGQRRLADFGAARLASKGT 1400

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Db	310	FTPEIQWTRRIILGLAVLHGRTNVHRIKGANILFK-----	347
QY	1401	GAGEFGQLLGTIAAPPELVLRGQ-YGRSGCVSVSCGAILIIMACAKPPMNHEKSHNHLA	1459
Db	348	-----GSPYMAAPREVVMGQNGYTHAVDYMISLGCITILEMATSKEPWS---QREGVGA	394
QY	1460	LIEKIASATTAIPSPHSPLGRDVALKRLLEQPODRSPRELIKKHPVRRTT	1511
Db	395	ALFKGNSKDPIELDPDHSNDANKETRLCLQNNPVYRPASQLEHPPLRNT	446

RESULT 15  
T01833

serine/threonine-specific protein kinase ARA.KIN (EC 2.7.1.-) - *Arabidopsis thaliana*  
N:Alternate names: protein T15F16.5

C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Data: 36-Feb-1998 #Accession number 36-Feb-1998

C:\Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 24-Sep-1999  
C:\Accession: T01833; S65789

R;Antoniou, B.; Le, T.  
submitted to the EMBL Data Library, August 1998

A;Description: The sequence of A. thaliana T15F16.  
A;Reference number: 21443

A;Accession: T01833

```
A;Status: translated
A;Molecule type: DNA
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A;Residues: 1-608 &lt;ANT&gt;

A; cross-references: EMBL:AF016275; NID:g33293582; PIDN:AAC28196.1; PID:g33377823  
A; Experimental source: cultivar Columbia

R;Cov1c, L.; Lew, R.R.  
B1ochim. B1ophvs. Acta 1305: 125-129, 1979

A/Title: Arabidopsis thaliana cDNA isolate

A;Accession: S65789  
A;Reference number: S65789; MUID:96180314; PMID:8597596

A: Molecule type: mRNA  
A: Residues: 'YVRE', 119-236, 'LDPLLTIGDRIG', 248-338, 'V', 340-358, 'G', 360-369, 'EVEALKNPYNRRC'

A: Cross-references: EMBL: L43125; NID: g871811; PIDN: AAA99196.1; PID: g871812

A;Map postt

A; Introns: 353/2; 381/3; 402/3; 455/2; 479/3; 499/3; 537/3  
A; Note: T15F16.5

**C/Superfamily:** unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homologs

F331-587/Domain: protein kinase homology <KIN>

F;339-347/Region: protein kinase ATP-binding motif

Query Match 5 98: Score 461 5: DB 2: Length 608-

Best Local Similarity 31.6%; Pred. No. 1.7e-09;  
Watchdog 118.0; Generated 118.0; Watchdog 118.0

Malices 18; Conservative 66; Mismatches 154; Indels 35; Gaps 12,

QY 1142 SSDTVTFRSEVAVLSPEKAENDTYKDDVNHNOCKREKMEAEIEEEALAIAMASASQDA 120

Db 246 SWDPLTHFASFMVKRPSSSSSSSS--EDGDEEEGKFEERARAREMGARETOLSDTADETC 303

[illegible]

09 1202 LF1VFQLEVENED111100D1PE1LPGHIKANQPIREDTEWLNKGQ01G1GAFSSC0YQ0 1202

Db 304 -----SFTTNEGDDSSSTVSNTSPIYPDGGAI-----TSWQKQGLGRGSGVSEGI 351

QY 1262 DVGIGTMAVKQVTVYRNTSSSEQEEVVEALREIRMSHLNHPNIRMLGATCEKSNYL 1321

Db 352 S-GDGFPAVKEVSL-DGSGAQECIQLEGEIKLISQLQHNTVRYRGTAKDGSNLYI 409

QY 1322 FIEMAGGSVAHLISKYGAFKESVINYTEOLLRGLSYLHENOI IHRDVKGANLLIDSTG 1381

410 FLEIWTGSLIKIYORV-OI BDSVSVI YTBOTI DCI KVI LNDCEI TDTKANTIVANC 469

[illegible]

```

0Y      I38Z QRLRIADIGAAARLASKGIGAGEEG--QLLGTLAFNAPEVLRGGQ---IGRSCDWSVSG 1436
          ::::| | | | | :| | | | | :| | | | |

```

Db 469 -AVKLADEGLAK-----VSKFNDIKSKCGTPFWMAPEVINRKDSDDGYGSPADIMSLG 519

QY 1437 CAIEMACAKPPWNAEKHSNHLIFKIASATTAPSTPSHLSPGLRDVALRCLELOPDR 1496

Db 520 CTVLEMGIGIPYS---DLEPVQALFRIGRG-TLPEVPDTLSLDARLFLIKCLKVNPEER 575

```
QY 1497 PPSRELLKHPPER 1509
      | : ||| | |
Db 576 PTAAEELLNHPFVR 588
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Search completed: December 20, 2002, 16:23:02  
Job time : 51 secs



QY	236	VQNSAASPASKGRSPSPGNSPGRNTYKSSSPGVRRKRRSPVPFQSGRTTPRRAPSPDG	295
Dd	231	GQAGSAAAPGGRKSPSPGSSPSGRVYKPPSPVPYRRKRVSPVFGSGRTTPRRAPSPDG	290
QY	236	FSPSPPEETNRVVKVYKARLYLLQOIGPMSPLIGDGPONKRYVIGQONSCARGPC	355
Dd	291	FSPSPPEETSRVVKYKARLYLLQOIGRMSPLIGDSDPNKRYVIGQONSCARGAF	350
QY	336	IHLFVMLRVQLEPSPDMLRKTLKMFVEVSLPKYXHSRISRKAPSRNTIQFVSRM	415
Dd	351	IHLFVMLRVQLEPSPDMLRKTLKMFVEVSLPKYXHSRISRKAPSRNTIQFVSRM	410
QY	416	SNSHTLSSSTSSSENSIKDEEOMCPICLLGMIDESITVCEGCGNKKLHHHOMSTW	475
Dd	411	SNSHTLSSSTSSSENSIKDEEOMCPICLLGMIDESITVCEGCGNKKLHHHOMSTW	470
QY	476	AEECRNRNEPLICLCSKMSKMSHDFYSHELSPVSDSPSLRAAOQOTVQOPLAGS-RRN	534
Dd	471	AEECRNRNEPLICLCSKMSKMSHDFYSHELSPVSDSPSLRAAOQOTVQOPLAGS-RRN	530
QY	535	QESNPNLHVCTOQIPRAYDIAEPMTQVYGMELVOCLEFSRMNNVEMALRRLSHDYSGA	594
Dd	531	QESNPNLHVCTOQIPRAYDIAEPMTQVYGMELVOCLEFSRMNNVEMALRRLSHDYSGA	590
QY	595	LLANGESTGNSGGSSSPSGCATSGSSQTSISGQVVEACGSVLSMPCADVYKYVYAA	654
Dd	591	LLANGESTGNSGGSGGSLSAGASGSSQPSISGQVVEACGSVLSICADVYKYVYAA	650
QY	655	LKTLRAMVYTPCHSLAEIRIKLQRLQOPVDTILVYCADANSTQSLSITLLELCQGA	714
Dd	651	LKTLRAMVYTPCHSLAEIRIKLQRLQOPVDTILVYCADANSTQSLSITLLELCQGA	710
QY	715	GELAVGREILKAGSIGIGQVDVYLCNLTICQOTESNNMOELLGLTCLIDBLEPFAEP	774
Dd	711	GELAVGREILKAGSIGIGQVDVYLCNLTICQOANSNMOMELGLTCLIDBLEPFAEP	770
QY	775	HIVSTDVQAEPVIRIKKLILTLTFLMOSINDSHSNVCKLSRRYTLSSARVTVPHVF	834
Dd	771	HIVSTDVQAEPVIRIKKLILTLTFLMOSINDSHSNVCKLSRRYTLSSARVTVPAVVF	830
QY	835	SKLEEMSVSSESTFTYHMRRLMAIDEVYIAIAIOLGVEDTIGQODSEFLQASVPNYLT	894
Dd	831	SKLTVMNLNASSHTFTYHMRRLMAIDEVYIAIOLGVEDTIGQODS-LQAVAPTSOL	889
QY	895	ETTENSPECTVHLEKTKGKLCATKLSASEDISERIASISVGPSSSTTTTTTTEOPK	954
Dd	890	---ENSSLEHTVHREKTKGKLSATRLSASEDISDRLSAGVGLPS---TTTEOPK	941
QY	955	MYOTKGRPHSOCUNSPSLSHSQLOMPALSTPSSSTPVPAGIADVCKHRLQIGTIPCR	1014
Dd	942	AVOTKGRPHSOCUNSPSLSHSQLOMPALSTPSSSTPVPAGIADVCKHRLQIGTIPCR	995
QY	1015	PSASPOTORKRSLOFHNRCPEKNDOKLSAEVTFQSPAPRLPSSNIHHPKPSRPPTKOSG	1074
Dd	996	PSASPOTORKRSLOFHNRCPEKNDOKLSAEVTFQSPAPRLPSSNIHHPKPSRPPTKOSG	1055
QY	1075	DPKSNKMTLDLNSSCKDDDFCGSSNNSNAVPSDETFTVPYBEKCRLDVNTLNSSTED	1134
Dd	1056	DATSSMTLDLGSASRCKDDDFCGSGGNSGNAVPSDETFTVPYBEKCRLDVNTLNSSTED	1115
QY	1135	LLEASMPSSDPTVYFKSEVAVLSPKRAENDYTKADOVNNOCCKEMEAEEFEALATAMA	1194
Dd	1116	LLEASMPSSDPTVYFKSEVAVLSPKRAENDYTKADOVNNOCCKEMEAEEFEALATAMA	1175
QY	1195	MSASODALPIVPOLOVENGEDIIITQODPPELPGHTKAKOPYREDTWMLKQOIGLGA	1254
Dd	1176	MSASODALPIVPOLOVENGEDIIITQODPPELPGHTKAKOPYREDAEWMLKQOIGLGA	1235
QY	1255	SSCQOADVCGITLMAKYOTVYRNSSSBOEEVEALREIIMSHLNPNITIRMLGATC	1314
Dd	1236	SSCQOADVCGITLMAKYOTVYRNSSSBOEEVEALREIIMSHLNPNITIRMLGATC	1295
QY	1315	EKSYNLFIEMMAGSVANHLSTYGAFKSEVAVNTYEQLLRSLSTYHEHQIITHRPVKAN	1374

	Db	1296	EKSNNLFIEMWAGGVAAHLILSKYGFKFSVVIINTYEOLRLRGSLYLHENQIITHRDVKGAN	1355
Oy	1375	LUIDSTGQLRIADFCFAARILASKGTGAEEFQGOLLGITAFAPMAPEVLRCGOQGRSCDWS	1434	
Db	1356	LUIDSTGQLRIADFCFAARILASKGTGAEEFQGOLLGITAFAPMAPEVLRCGOQGRSCDWS	1415	
Oy	1435	VCCALITEMACAKPMPWAEXHSHNLALIFKIASATTAPASIPSHLSPLRDLVALRCLELOPO	1494	
Db	1416	VCCALITEMACAKPMPWAEXHSHNLALIFKIASATTAPASIPSHLSPLRDLVALRCLELOPO	1475	
Oy	1495	DRPPSRELLKHPEVRTTW 1512		
Db	1476	DRPPSRELLKHPEVRTTW 1493		
	RESULT 2			
	US-10-000-864-8			
	; Sequence 8, Application US/10000864			
	; Patent No. US20020146798A1			
	GENERAL INFORMATION:			
	; APPLICANT: CADUS PHARMACEUTICAL CORPORATION			
	; TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES			
	; TITLE OF INVENTION: AND USES THEREFOR			
	; FILE REFERENCE: CPI-085CPC			
	; CURRENT APPLICATION NUMBER: US/10/000,864			
	; CURRENT FILING DATE: 2001-10-31			
	; EARLIER APPLICATION NUMBER: 09/423,890			
	; EARLIER FILING DATE: 2000-06-03			
	; EARLIER APPLICATION NUMBER: PCT/US99/05556			
	; EARLIER FILING DATE: 1999-03-15			
	; EARLIER APPLICATION NUMBER: USSN 60/078,153			
	; EARLIER FILING DATE: 1998-03-16			
	; EARLIER APPLICATION NUMBER: USSN 60/099,165			
	; EARLIER FILING DATE: 1998-09-04			
	; NUMBER OF SEQ ID NOS: 38			
	; SOFTWARE: PatentIn Ver. 2.0			
	; SEQ ID NO 8			
	; LENGTH: 1493			
	; TYPE: PRT			
	; ORGANISM: Mus musculus			
	US-10-000-864-8			
	Query Match	88.3%; Score 6912.5; DB 12; Length 1493;		
	Best Local Similarity	89.5%; Pred. NO. 0;		
	Matches 1358; Conservative	47; Mismatches 82; Indels 31; Gaps 11		
Oy	1	MAAAGNRASSSGFGARATSPDA---GGGGALKRASSAPAA--AAGLIREAGSGGERAD	56	
Db	1	MAAAGNRASSSGFGARATSPDA---GGGGALKRASSAPAA--AAGLIREAGSGGERAD	60	
Oy	57	WRRLQLRKRSVELLOLPPOPFLF--AAPASTSTSPRPADAAGSGTGFQVAAPPBP	115	
Db	61	WRRLQLRKRSVELLOLPPOPFLF--AAPASTSTSPRPADAAGSGTGFQVAAPPBP	120	
Oy	116	AASRGCAHTESVAAPDGCASSPAAPAEPEGKRAPAAPSPSPAAPAGREMENKETIKGLHK	175	
Db	121	AASRGCSHAETLAARDSGARSAPAAGEP-----PS-AAAPSGREMENKETIKGLHK	170	
Oy	176	MDDREERNIRKTLKATCPAPMKHMLERNRNGVVYVPITVKDGSEPMNLIAESPDE	235	
Db	171	MEDREERNIRKTLKATCPAPMKHMLERNRNGVVYVPITVKDGSEPMNLIAESPDE	230	
Oy	236	VOASAASPASKGRSPSPGNSSPGRTVASESPGVRRKRKRVPPFPQSGRTTPPRRAPSPDG	295	
Db	231	GQAGSAAPAPKGRSPSPGSVSGRSVKRESPGVRRKRKRVPPFPQSGRTTPPRRAPSPDG	290	
Oy	296	FSPYPPEETNRNVKNMARLYLLQOIGPNRLFJGDSPDNKYRYFIFGQNQSCARGTFC	355	
Db	291	FSPYPPEETSRRVNVKMARLYLLQOIGNSFLLJGDSPDNKYRYFIFGQNQSCARGTFC	350	
Oy	356	IHLTVMLRVFPLEBDSPLMKTKLNFVEEELFOKYHSRRSRIRKAPRNITQKFVSM	415	

Db 351 IHLFWMLRNFQLEPSPDPMILMRKTLKNEFVESILFQKYHSRRSRIKAPSRNTIOKPFVSRM 410  
QY 416 SNHSTLSSSTSTSSSENSIKDEEOMCPICLLGMLDEESLTVCEDCGRNKLHHHCSIW 475  
Db 411 SNHSTLSSSTSTSSSENSIKDEEOMCPICLLGMLDEESLTVCEDCGRNKLHHHCSIW 470  
QY 476 AEECRNRREPLICPLCRSKRSHDFYSHELSSPYVDSPLRAAOQVVOOPLAGS -RRN 534  
Db 471 AEECRNRREPLICPLCRSKRSHDFYSHELSSPYVDSPLRAAOQVVOOPLAGS -RRN 530  
QY 535 QESNPNLTHGTQOIPPAYDIAEPWIOVGMELVCLFRRNNVVRMALRRLSHDVSQA 594  
Db 531 QESNPNLTHGTQOIPPAYDIAEPWIOVGMELVCLFRRNNVVRMALRRLSHDVSQA 590  
QY 595 LLLANGESTGNSGGSSSGSGATSSGOTSISGDVVEACCSVLSMVCADPYKVVYAA 654  
Db 591 LLLANGESTGNSGGSSSGSGATSSGOTSISGDVVEACCSVLSMVCADPYKVVYAA 650  
QY 655 LKTLRAMLVTPCHSLAERIKLQRLQPVVDIILVVCADANSRISQSLSTLELCKGOA 714  
Db 651 LKTLRAMLVTPCHSLAERIKLQRLQPVVDIILVVCADANSRISQSLSTLELCKGOA 710  
QY 715 GELAVGREILKAGSIGIGVDYVLCILGNOTESNNMOELLGRCLIDRLLEPFAEFP 774  
Db 711 GELAVGREILKAGSIGIGVDYVLCILGNOTESNNMOELLGRCLIDRLLEPFAEFP 770  
QY 775 HIVSTVSOAPEVEIRKYLKLLSTLFALQSIDNSHSMVGLSRRIYLSARMTVTVHF 834  
Db 771 HIVSTVSOAPEVEIRKYLKLLSTLFALQSIDNSHSMVGLSRRIYLSARMTVTVHF 830  
QY 835 SKLEMLSVSSSTHFTMRRLMAIADVEILAEIQLGVEDLIDGQDSFLQASVPNNYL 894  
Db 831 SKLVMTMLNAGSTHFTMRRLMAIADVEILAEIQLGVEDLIDGQDSFLQASVPNNYL 889  
QY 895 ETTENSPECTVHLEKTKGICATKLSASEDISERLASISVGSPSTTTTTEDEPKP 954  
Db 890 ---ENSLFHTVIRETKGKLSATRLSASEDISERLASISVGSPSTTTTTEDEPKP 941  
QY 955 MVOTKGRPHSOCNSPFLSHSOLMPALSTPSSSTPSPVAGTADYVKHRLQGFICRI 1014  
Db 942 MVOTKGRPHSOCNSPFLSHSOLMPALSTPSSSTPSPVAGTADYVKHRLQGFICRI 995  
QY 1015 PSASPOTQKRFSTQFHNCENKDSKLSPVFQSRPLPSSNTHRPSPRTPONTSKOG 1074  
Db 996 PSASPOTQKRFSTQFHNCENKDSKLSPVFQSRPLPSSNTHRPSPRTPONTSKOG 1055  
QY 1075 DPKNSTMTLNLSSSKCDDDFGCSNNSGNAVIPSDETVPFVEEKCKLDVTELNSSLED 1134  
Db 1056 DPKNSTMTLNLSSSKCDDDFGCSNNSGNAVIPSDETVPFVEEKCKLDVTELNSSLED 1115  
QY 1135 LLEBAMPSDDTVTFKSEVAVLSPEKAENDTYKDVNHNOKCKEKMABEEELATAMA 1194  
Db 1116 LLEBAMPSDDTVTFKSEVAVLSPEKAENDTYKDVNHNOKCKEKMABEEELATAMA 1175  
QY 1195 MSASODALPVPOLOVNGEDIIITQODTPETLPGHTKAKOPRYEDTEWLKGOIGICAF 1254  
Db 1176 MSASODALPVPOLOVNGEDIIITQODTPETLPGHTKAKOPRYEDTEWLKGOIGICAF 1235  
QY 1255 SSCYOADVGTGLMAKQVTVYRNTSSBOEVEYALREIRBMASHNHPITMLGATC 1314  
Db 1236 SSCYOADVGTGLMAKQVTVYRNTSSBOEVEYALREIRBMASHNHPITMLGATC 1295  
QY 1315 EKSNTYLFIEEMAGGVANHLISKYAFKESVVIYNTBOLRGLSYLHENQIIRHDVGAN 1374  
Db 1296 EKSNTYLFIEEMAGGVANHLISKYAFKESVVIYNTBOLRGLSYLHENQIIRHDVGAN 1355  
QY 1375 LLLDSTQORIRIADFGAAALASGTGAGEFOGLTIAFMAEYVRGOQYGRSCVWS 1434  
Db 1356 LLLDSTQORIRIADFGAAALASGTGAGEFOGLTIAFMAEYVRGOQYGRSCVWS 1415  
QY 1435 VGCATIEMACAKPPWNAEKSHNLALFKTASATTAISPSHSPGLRDVALRCLLEPO 1494  
Db 1416 VGCATIEMACAKPPWNAEKSHNLALFKTASATTAISPSHSPGLRDVALRCLLEPO 1475

QY 1495 DRPPSREILKHPVETTW 1512  
Db 1476 DRPPSREILKHPVETTW 1493  
RESULT 3  
US-09-858-754-4  
; Sequence 4, Application US/09858754  
; Patent No. US20020055130A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Gary L.  
; TITLE OR INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS  
; FILE REFERENCE: CFI-042  
; CURRENT APPLICATION NUMBER: US/09/858,754  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/023,130  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/039,740  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1493  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-858-754-4

Query Match 88.1%; Score 6892.5; DB 10; Length 1493;  
Best Local Similarity 89.2%; Pred. No. 0;  
Matches 1350; Conservative 45; Mismatches 96; Indels 23; Gaps 8;

QY 1 MAAAGNRASSSGFPAGATSPKAGGGGALKASAPAAAGLTLREAGSGGERADWRR 60  
Db 1 MAAAGNRASSSGFPAGATSPKAGGGGALKASAPAAAGLTLREAGSGGERADWRR 60  
QY 61 QLRKRVSYELDQLEPQPLFLASPPASTSPSPEDADAGSGTGFPVAPPPHGAASRG 120  
Db 61 QLRKRVSYELDQLEPQPLFLASPPASTSPSPEDADAGSGTGFPVAPPPHGAASRG 120  
QY 121 GAHLETSVAAPDSCASSPAAPEPKRPAAPSPAAAPAGREMKETLGLHKMDRP 180  
Db 121 GSHAEILAAADSGARSPAGAP-----PS-AAAPSGREMKETLGLHKMDRP 170  
QY 181 EEMIRREKATKAPAMKHEWLERNNRGPVYVPIPKGSGSEMNHILAAESPGVQASA 240  
Db 171 EEMIRREKATKAPAMKHEWLERNNRGPVYVPIPKGSGSEMNHILAAESPGVQASA 230  
QY 241 ASPASKGRSPSPGNSPGRTVKSESPGVRRKRVSPVPFQSGRTTPPRASPDPGFSYS 300  
Db 231 AAPAPKGRSPSPGNSPGRTVKSESPGVRRKRVSPVPFQSGRTTPPRASPDPGFSYS 290  
QY 301 PEENRRNRKMYRRLYLQOIGPNSFLIGDSDPNKRYVITGPNCSAGACTCIIHLLF 360  
Db 291 PEETSRNRKMYRRLYLQOIGPNSFLIGDSDPNKRYVITGPNCSAGACTCIIHLLF 350  
QY 361 VMLVFOLEPDPMLMRKTLKNEFVESILFQKYHSRRSRIKAPSRNTIOKPFVSRM 420  
Db 351 VMLVFOLEPDPMLMRKTLKNEFVESILFQKYHSRRSRIKAPSRNTIOKPFVSRM 410  
QY 421 LSSSSTSTSSSENSIKDEEOMCPICLLGMLDEESLTVCEDCGRNKLHHHCSIAEBCR 480  
Db 411 LSSSSTSTSSSENSIKDEEOMCPICLLGMLDEESLTVCEDCGRNKLHHHCSIAEBCR 470  
QY 481 RNRREPLICPLCRSKRSHDFYSHELSSPYVDSPLRAAOQVVOOPLAGS -RRN 539  
Db 471 RNRREPLICPLCRSKRSHDFYSHELSSPYVDSPLRAAOQVVOOPLAGS -RRN 530  
QY 540 NLTHYGTQOIPPAKDLAEPWIOVGMELVCLFRRNNVVRMALRRLSHDVSQALILAN 599  
Db 531 NLTHYGTQOIPPAKDLAEPWIOVGMELVCLFRRNNVVRMALRRLSHDVSQALILAN 590  
QY 600 GESTGNSGSGSSPSCGATSGSSOTSISGDVVEACCSVLSMVCADPYKVVYAA 659

591 AMLVTPCHSLAERIKLQRLQPVDTILVKCADANSRTSOLISTLLELCCKGAGELAV 650  
660 AMLVTPCHSLAERIKLQRLQPVDTILVKCADANSRTSOLISTLLELCCKGAGELAV 719  
651 AMLVTPCHSLAERIKLQRLQPVDTILVKCADANSRTSOLISTLLELCCKGAGELAV 710  
720 GREILLKAGSIGGVYVNCILGNOTESNNMQLLGRCLDLRLLEPAEYPIHVST 779  
711 GREILLKAGSIGGVYVNCILGNOTESNNMQLLGRCLDLRLLEPAEYPIHVST 770  
780 DVSQAEPEVIRKRLSLTLTALQSDIDNSHWGKLSRRITLSSARWVTPVHVSFLE 839  
771 DVSQAEPEVIRKRLSLTLTALQSDIDNSHWGKLSRRITLSSARWVTPVHVSFLE 830  
840 MLSVSSSTHTNRRRLMAIADEVEIAEALQLGVEDTLGQODSFLQASVPNNYLETTEN 899  
831 MLSVSSSTHTNRRRLMAIADEVEIAEALQLGVEDTLGQODSFLQASVPNNYLETTEN 886  
900 SSPCTVHLEKTKGKCAKRLSSSEDISERLASISVG-PSSSTTTTTTTTTEOPKPMVOT 958  
887 SLEHTAHVEKTKGKCAKRLSSSEDISERLASISVG-PSSSTTTTTTTTTEOPKPMVOT 940  
959 KSRPHSQCINSSPLSHSOLMFPALSTPSSSTPVAGTATDYSKHRLQGFICRIPAS 1018  
941 KSRPHSQCINSSPLSHSOLMFPALSTPSSSTPVAGTATDYSKHRLQGFICRIPAS 999  
1019 POTOQKFSIQFHRCNCPENKDSKLSFVFTQSRPLSSNTHRPKSPRPGNTSKODPSK 1078  
1000 POTOQKFSIQFHRCNCPENKDSKLSFVFTQSRPLSSNTHRPKSPRPGNTSKODPSK 1059  
1079 NMTDLNNSKRCDSFGGSSNSNAVIPSDEVFVTPVEKGLDVTLENSIEDLLER 1138  
1060 NMTDLNNSKRCDSFGGSSNSNAVIPSDEVFVTPVEKGLDVTLENSIEDLLER 1119  
1139 SMPSSDTVTTFKSEVAVLSPKAEANDTYKDDVNHQCKEKEAESEALATAMASAS 1198  
1120 SMPSSDTVTTFKSEVAVLSPKAEANDTYKDDVNHQCKEKEAESEALATAMASAS 1179  
1199 ODALPIVPOLOVENGEDIIIIODPIPETLPHTKAKOPYREDTEMLKGOOIGLAFSSCY 1258  
1180 ODALPIVPOLOVENGEDIIIIODPIPETLPHTKAKOPYREDTEMLKGOOIGLAFSSCY 1239  
1259 QADODGTGLMAVKQVTVYRNTSSQEEVEVALREIRMSHNLNHNITRMGATEKSN 1318  
1240 QADODGTGLMAVKQVTVYRNTSSQEEVEVALREIRMSHNLNHNITRMGATEKSN 1299  
1319 YMLFTEWMAAGSVAILSKYGAFFKESVINTYEQLLRGSLYHENOIIHRDYGANLLID 1378  
1300 YMLFTEWMAAGSVAILSKYGAFFKESVINTYEQLLRGSLYHENOIIHRDYGANLLID 1359  
1379 STGQRLRIADFGAARLASKGTGAGEFQGLGTIAFMAPEVLRGQOYGRSCDWSVGCA 1438  
1360 STGQRLRIADFGAARLASKGTGAGEFQGLGTIAFMAPEVLRGQOYGRSCDWSVGCA 1419  
1499 IEMCAKPRMAEKHSNHLALIFKIASATTPASTPSHLSFGLRDVALMCLBOPDRP 1498  
1420 IEMCAKPRMAEKHSNHLALIFKIASATTPASTPSHLSFGLRDVALMCLBOPDRP 1479  
1499 SRELLKHPVFTTW 1512  
1480 SRELLKHPVFTTW 1493

RESULT 4  
US-10-000-864-2  
: Sequence 2, Application US/10000864  
: Patent No. US20020146798A1  
: GENERAL INFORMATION:  
: APPLICANT: CADUS PHARMACEUTICAL CORPORATION  
: TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES  
: FILE REFERENCE: CPT-085CPC

CURRENT APPLICATION NUMBER: US/10/000,864  
: EARLIER FILING DATE: 2001-10-31  
: EARLIER APPLICATION NUMBER: 09/423,890  
: EARLIER FILING DATE: 2000-06-03  
: EARLIER APPLICATION NUMBER: PCT/US99/05556  
: EARLIER FILING DATE: 1999-03-15  
: EARLIER APPLICATION NUMBER: USSN 60/078,153  
: EARLIER FILING DATE: 1998-03-16  
: EARLIER APPLICATION NUMBER: USSN 60/099,165  
: EARLIER FILING DATE: 1998-09-04  
: NUMBER OF SEQ ID NOS: 38  
: SOFTWARE: Patentln Ver. 2.0  
: SEQ ID NO 2  
: LENGTH: 1302  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-10-000-864-2

Query Match 80.7%; Score 6318.5; DB 12; Length 1302;  
Best Local Similarity 93.4%; Pred. No. 0;  
Matches 1230; Conservative 26; Mismatches 46; Indels 15; Gaps 5;

196 AMKHEMLERNRRGPVYVRIPIYKGDGSENNHLAESPGEVQASASPASKGRSPGPN 225  
1 AMKHEMLERNRRGPVYVRIPIYKGDGSENNHLAESPGEVQASASPASKGRSPGPN 60  
256 SPGRTVYKSESPGRRKRVSPVPFQSGRTIPPRAPSPDGFSPSPETNRRNRYKVRAR 315  
61 SPGRTVYKSESPGRRKRVSPVPFQSGRTIPPRAPSPDGFSPSPETNRRNRYKVRAR 120  
316 LYLLQOIGRNSFLIGDSDPNKTRVITGPONCSGANGTFCILHLYVLRVQLEPSDPL 375  
121 LYLLQOIGRNSFLIGDSDPNKTRVITGPONCSGANGTFCILHLYVLRVQLEPSDPL 180  
376 WRKTLNFEVESLFQKYHSRSTRKAPSNRTOKFVSRMSNHTLSSSTSSSENST 435  
181 WRKTLNFEVESLFQKYHSRSTRKAPSNRTOKFVSRMSNHTLSSSTSSSENST 240  
436 KDEEQMCPICLLGMDLESLTVCEDCRNKLNHNCMSIWAECRRNRREPLICPLCRSKW 495  
241 KDEEQMCPICLLGMDLESLTVCEDCRNKLNHNCMSIWAECRRNRREPLICPLCRSKW 300  
496 RSHDFYSHELSPVDSPTSLRAAQOQTVQOPLAGSRNDSFNLTHTGTQOIPPAVKD 555  
301 RSHDFYSHELSPVDSPTSLRAAQOQTVQOPLAGSRNDSFNLTHTGTQOIPPAVKD 360  
556 LAEPWIOVFGMELVGLFESNNMVRMALRLSHDVSAGALLANGSTGSSGSSSPS 615  
361 LAEPWIOVFGMELVGLFESNNMVRMALRLSHDVSAGALLANGSTGSSGSSSPS 420  
616 GCATSGSQTSISGDVVEACCSVLSHWACADPVYKVVVAALKTPLRAMLVYTPCHSLAERIK 675  
421 AGAASSSQPSISGDVVEACCSVLSHWACADPVYKVVVAALKTPLRAMLVYTPCHSLAERIK 480  
676 LQRLQPVDTILVKCADANSRTSOLISTLLELCCKGAGELAVREILLKAGSIGGVYD 735  
481 LQRLQPVDTILVKCADANSRTSOLISTLLELCCKGAGELAVREILLKAGSIGGVYD 540  
736 YVNCILGNOTESNNMQLLGRCLDLRLLEPAEYPIHVSTVDSQAEPEVIRKRL 795  
541 YVNCILGNOTESNNMQLLGRCLDLRLLEPAEYPIHVSTVDSQAEPEVIRKRL 600  
796 SLTFLALQSDIDNSHWGKLSRRITLSSARWVTPVHVSFLEMLSVSSSTHTNRRRL 855  
601 SLTFLALQSDIDNSHWGKLSRRITLSSARWVTPVHVSFLEMLSVSSSTHTNRRRL 660  
856 LMAIADEVEIAEALQLGVEDTLGQODSFLQASVPNNYLETTENSSPECTVHLEKTKGL 915  
661 LMAIADEVEIAEALQLGVEDTLGQODSFLQASVPNNYLETTENSSPECTVHLEKTKGL 716  
916 CATKLSASSEDISERLASISVGSSSTTTTTTTTTEOPKPMVOTKGRPHSQCINSSPLSH 975  
717 SATRLSASSEDISERLASISVGSSSTTTTTTTTTEOPKPMVOTKGRPHSQCINSSPLSH-H 770

Qy	976	SQMFPLPSTSSSTPVGATDYSKRIJOFICRILPMSAPOTORFSLQFHRNPE	1035
Db	771	QOLMFPPASAPCSSASVP-----DISKHPQAFVPCKIPSPQORNFSLQFORNCE	825
Qy	1036	NKDSDKLSPFTOSRPLPSSNIHRPKPSRPTGANTSKODPASKNMTLDLNSSKCDOSF	1095
Db	826	HRSDQILSPVFTQSRPPSSNIHRPKPSRVPGSTISLGDARKSMITLDLSGASKCDOSF	885
Qy	1096	GCSSNSSNAVIPSDFTVFTPEVEEKCRLDVNTELNSSIEDLLEASMPSSDTVTTFKSEYAV	1155
Db	886	GGGSGNSNAVIPSDFTVFTPEVEDKCRLDVNTLENSSIEDLLEASMPSSDTVTTFKSEYAV	945
Qy	1156	LSPEKANDOTTYKDDVHNHCKCKEKEAEBEELAIATAMMSASODALPIVPOLOVENGD	1215
Db	946	LSPEKANDOTTYKDDVHNHCKCKEKEAEBEELAIATAMMSASODALPIVPOLOVENGD	1005
Qy	1216	IIIIIOQOTPELPEGHTAKOPYREDIEMTKGQOIGGAFSSCYOQADVGITGLMVKQYT	1275
Db	1006	IIIIIOQOTPELPEGHTAKOPYREDIEMTKGQOIGGAFSSCYOQADVGITGLMVKQYT	1065
Qy	1276	YVRNTSSEOEVEALKEELIRMSHNLHPNIIITMLGATEKSNYMLFIEMMAGGSVAHL	1335
Db	1066	YVRNTSSEOEVEALKEELIRMSHNLHPNIIITMLGATEKSNYMLFIEMMAGGSVAHL	1125
Qy	1336	SKYAFKESYVINTTEOLLGSLYLHENDIIRHDYKGANLLIDSTGQRLIADFGAARL	1395
Db	1126	SKYAFKESYVINTTEOLLGSLYLHENDIIRHDYKGANLLIDSTGQRLIADFGAARL	1185
Qy	1396	ASKGTGGEFQGLGIIAMAEVYLRGOOYGRSCYWSYGCAIITEMACAKPPMAEKHS	1455
Db	1186	ASKGTGGEFQGLGIIAMAEVYLRGOOYGRSCYWSYGCAIITEMACAKPPMAEKHS	1245
Qy	1456	NHLILIKISATAPSIPIHSLBGLRDVALRCLTELQOPDRPSPREILKHPFERITW	1512
Db	1246	NHLILIKISATAPSIPIHSLBGLRDVALRCLTELQOPDRPSPREILKHPFERITW	1302

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RESULT 5
US-09-858-754-5
Sequence 5, Application US/09858754
Patent No. US20020055130A1
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS
FILE REFERENCE: CRI-042
CURRENT APPLICATION NUMBER: US/09/858,754
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/023,130
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/039,740
PRIOR FILING DATE: 1997-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 1034
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Xaa's at positions
OTHER INFORMATION: 19,20,30,52-55,57,58,60,61,68,159,164,174-305,336,
OTHER INFORMATION: 339,341,344,351,353,355,375,519,555,556,691,692,693,
OTHER INFORMATION: 5-739,767,769,777-814,819,827,834,842,864,870,875
OTHER INFORMATION: and 890 may be any amino acid
OTHER INFORMATION: Xaa's at positions 901,904,916,922,932,943,946,
US-09-858-754-5

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Query Match	40.9%	Score 3200;	DB 10;	Length 1034;
Best Local Similarity	64.3%	Pred. No. 3.8e-162;		
Matches 677;	Conservative 25;	Mismatches 325;		
			Indels 26;	Gaps 9

QY 465 NKLHHCMSIWAEECRNRREPLICPLCRSKWRSHDFYSHELSSPYVDSPPSLRAAQQTVO 524

Db	1	NKLHHCMSTIAEECRXNNXXPLICPLCRSGMSHDPYSHELSSPVDSPSSLLXXXXXXVX	60
QY	525	QOPLAGS-RRNOSNENLHYGTQOIPPAYKDLAEPIOVFEMELVGLFSRNNVREMA	583
Db	61	XHPLAGSXRRROESNFULHYGTQOIPPAYKDLAEPIOVFEMELVGLCFRNNVREMA	120
QY	584	LRLSHVSGALLLANEESTGNSGSSGSSPGSGATSSGSORTSIGDVEVACCVLSMYC	643
Db	121	LRLSHVSGALLLANEESTGNSGSSGSSPGSGATSGASOTXSJGDVVEACCVXXXXXX	180
QY	644	ADPYKYVAALXTLRAMLVYTPCHSLAEIRIKLQRLLOPVDTIIVKCADANSRTQLSI	703
Db	181	XX	240
QY	704	STLELCKGAGELANGREILKAGSIGIGVDYVLCILIGNOTESNMOELLGRCLIDR	763
Db	241	XX	300
QY	764	LLEPFAEPHYSTVDVSOAPEVLEIRYKLLSLTLFALQSDNHSWAGKLSR---I	819
Db	301	XXXXXXXXPEEPHYSTVDVSOAPEVLEIRYKLLSLTLFALKXIDSHSWAGXSRDLSL	360
QY	820	YLSARWYTVPHVFSKLEMLSVSSSTFHTRRRLMAIADEVEIAAIOLOGVEDTLDG	879
Db	361	CYDDGRSAVCEP---SMXCMKLDSHTFHTRRRLMAIADEVEIAAIOLOGVEDTLDG	416
QY	880	QOOSFLQAVPNVYLETTEENSPECTVHLKCTGKLCATKLSASSEDISERLASVQ-P	938
Db	417	HQDS-LRALAP---ASCRENSSLEHYHREKTKGLSATRLSTSEEISDRLAGSVGEP	472
QY	939	SSSTTTTTTEQRPVWQYKGGPHQOCNSSLSHSQDLMRPALSTSSSTPSVPACTA	998
Db	473	SS-----TTEDQRPVWQYKGGPHQOCNSSLSPS-HAQMLPAVSACSSAPVXP----	521
QY	999	TDVSKHRLQGIPIRIPASAPOTQRFKFSLOFHNCPCENDOSPKLSPVYOTOSAPLPSNIH	1058
Db	522	-DISKHPQAFVPEKILPHLPOTQRFKFSLOFHNCPCENDOSPKLSPVYOTOSAPLPSNIH	580
QY	1059	RPKPSRPTPGNTSKQGDPSKNSMTLIDNSSKCDSEFGSSNSSNAVIPSEVTFPYEE	1118
Db	581	RPKPDRAPGSGSTKLGATKSSMTLIDGOCSCDSEFGGSGNSGNAVIPSEVTFPYED	640
QY	1119	KCRLDVTELNSSSTEDLLESMSPSPTTYTFKSEVAVLSEPEAENDDTYKDYVHNQCK	1178
Db	641	KCRLDVTELNSSSTEDLLESMSPSPTTYTFKSEVAVLSEPEAENDDTYKXXVYXXXXXX	700
QY	1179	EKMEAEHEELAIAIMASASODALPIVPOLOVYENGEDIIITIOODPPELTPGHTRAKOPYR	1238
Db	701	XXVIOODPPELTPGHTRAKOPYR	760
QY	1239	EDTEMLKGOOIGLGAFFSSCYOADVGTGLTLMAYKOYTVVRNTSSBOEEVVALREELRM	1298
Db	761	EDAEMLKGOOIGLGHFFXXEETX	820
QY	1299	SHLHNPINIRLGAETCKSKSYNLPFIEMAGGSVAHLSTYGFKFSYVINTEDLRLS	1358
Db	821	SHLHNPXIRLGLTKGKSKSYNLPFIEMAGGSVAHLSTYGFKFSYVIXYTEOLRLS	880
QY	1359	YLHENQIIRHVKCANLLIDSTGORLIDDFGAARLASKGAGEFOGLLGTATFAP	1418
Db	881	YLHENQIIRHADVKANLLIDXTGRRLRIADFGAAALASKGAGEFOGLXGTATFAP	940
QY	1419	EVLNGOQYGRSCDWVSVCALIEMACAKPPWNAEKSHNLALIFKIASATTAPISPHS	1478
Db	941	EYXGKQYGRSCDWVSVCALIEMACAKPPWNAEKSHNLALIKRIASATTAPISPHS	1000
QY	1479	PGLRDVALRCLLEIQPODRPSPRELKHPVFRIT	1511
Db	1001	PGLRNVALRCLLEIQPODRPSPRELKHPVFRIT	1033

## RESULT 6





Db 417 --SLPTSDKGNLM--NKFRRSQIGVSPNVAVTSSQ-----ETPSLK----SNSS 461  
QY 698 TSQSLSTL-----LELCQAGELAVGREILKAGSIGGVADVILCLIGN 744  
Db 462 TATLTVOATADVNIIPSSSPPIPKTANRSLVSTEDTETSTASFKETYPDCCINPD 521  
QY 745 QT---ESNNMOELLGRCLDLRLLEPPAFPHIYSTDVSOAE-----PV 787  
Db 522 KTVVPVNN--OKYSVKNFLLDQ-----KFYP-LKRTGLNDSBNXYLVTKDNVSEVPL 572  
QY 788 EIR-YKLLSLTFLFALOSINSHSMV-----GK 814  
Db 573 NLSVAKLSFKESALTKLILNKNVTFFHMTDPCDIGAALPDDTLEFLKSKLEFNTSGK 632  
QY 815 LSRRIYLSARWTVYVPHVSKLEMLSVSSSTHFTMRRLMAIADEVEIAEAIQ--LG 872  
Db 633 IYIKDQKLLQOKRPAPLVTENNVPILKSVKSSMRSGTSLASTDVSIVTSSDITS 692  
QY 873 VEDTLGQODSFLQASVPNNYLETENSSP-----ECYVLEKTKGKLCAT--KL 920  
Db 693 FDBHASSGSGRRYPQ--TPSYYYDRVSNTPTEELNWNINKEVLSHEBNAPRMVFKTSPKL 750  
QY 921 SASSEDSERLASISVSPSSSTTTTTTQPKPMVOTKGRPHSGCLNSS-----PLSHH 975  
Db 751 ELNLPKGSKL-----NIPPIITENESSKSPQYLKDEGTIDFNHR 792  
QY 976 SOLMF--PALSTPSSSPVSPAGATDVSKHRLQGFIPCRIPASPOTORKFSLOFHRNC 1033  
Db 793 RESPYRPELA--PKREAPKRPANTSPQRTLSTSKONKPIRLVASTYISRS-----842  
QY 1034 PENKSDKLSPVTTQSPRLPSSNHRP--KPSRPPGNTSKOGDPSKSMIL-----D 1084  
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QY 1085 LNSSSKCD--DSFGSS-----NSNAVIPSEVTF--TP-----VEEKRL 1122  
Db 890 VMRLKTDQDSTSTSPSLKQKQYKNSNVTSTNSITFSPSLKKNKRYVSTISAA 949  
QY 1123 DVNTELNSSIEDLLEASMP-----SSDTVTYKSEVAV-----LSPERAKN 1163  
Db 950 DIFEE--NDJTFADAPMFDDSDDDSSDDIIMSKKAPAFNENKDKEDSDN 1004  
QY 1164 DDTYKDVNINQCKEKN-----AEEELALAMASASODA 1201  
Db 1005 SSTHSDEIFYDSQODMERKMTFRPSPEVYVQMLEKFFPRANIDKPIITEGIASPTSPKS 1064  
QY 1202 L-----PIVQLOVE-----NGEDIIITQODTP-----1224  
Db 1065 LDSLSEKNVASSRTEPSTSPRPVPPDSSTYEFIODGLNGKKPLNOAKTPKRTKTITIA 1124  
QY 1225 -----ETLPQH--TKAKOPYREDE--WLKGOQIGLG 1252  
Db 1125 HEASLARKNSVKLRONTKMMGTMEVETENHWSINKAKNSKEVEKFAAMKEMKKG 1184  
QY 1253 AFSSCYAQOVGCTLMAVQVTVYRNTSSQOEVEY--VEALREIIMMSHLNPNITRM 1309  
Db 1185 SFGVYVYCLVWTTGEMMAVQVE--VPKSSQNEALISTVEALRESEVSTLKDLDHINTVOY 1243  
QY 1310 LGATCEKSN--YNLFEMMAGSVAHLISKYGAFKESVIVNTEOLLRGSLYHENQIHRD 1369  
Db 1244 LGFENKNNTISLPLEIYAGGSVGLIMYGFDEPLIKHLITVOYLGATYHSGILHRD 1303  
QY 1370 VKGANLLIDSTGQRLRIADFGAARLASKGTGAGEFOGOLLGTIAFMAPEVLRGOQY 1427  
Db 1304 MKADNLLDQDG--ICKISDPSIKRK--SKDIYSNS--DMTNGYVFWMAPEKVVDRKQGSA 1359  
QY 1429 SCQVWSYGCAIIEMACAKPPMAEKHSNHLALIFKIASATTAPSIPIHSLSGLDVALR 1487  
Db 1360 KVDIWSJGCTVLEMPACKRPPWS--NLEVYAAFMKIGKSKSAPPIDETPLPISQIGRNF 1416  
QY 1488 ---CLELOPQDRPPSRELLKH 1506  
Db 1417 LDACFEINPEKRPYANELLISHP 1438

RESULT 8  
US-10-000-864-12  
; Sequence 12, Application US/10000864  
; Patent No. US20020146798A1  
; GENERAL INFORMATION:  
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION  
; TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: CFI-085CPC  
; CURRENT APPLICATION NUMBER: US/10/000,864  
; CURRENT FILING DATE: 2001-10-31  
; EARLIER APPLICATION NUMBER: 09/423,890  
; EARLIER FILING DATE: 2000-06-03  
; EARLIER APPLICATION NUMBER: PCT/US99/05556  
; EARLIER FILING DATE: 1999-03-15  
; EARLIER APPLICATION NUMBER: USSN 60/078,153  
; EARLIER FILING DATE: 1998-03-16  
; EARLIER APPLICATION NUMBER: USSN 60/099,165  
; EARLIER FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 626  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-000-864-12  
  
Query Match 7.1%; Score 559; DB 12; Length 626;  
Best Local Similarity 29.9%; Pred. No. 1,6e-22;  
Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;  
  
QY 1016 SASPOTOKRFFSLQFHRNCPENKSDKLSPVTTQSPRLPSSN-----IHRKP-----1062  
Db 110 SSMKSLRIILLSDRN--HTSSPHSGVSRQYRIKPSQAGDINTIYQAPERSRLS 166  
QY 1063 -----SRPTG-----NTSKQDPSKNSMTIDLNSSKCDSDSFGCSSNSNAVIP 1107  
Db 167 VSSONPGRSSPPGVYPERQOHIARQ-----SYT-----SINSEGETIP 206  
QY 1108 SDEVTFTVEKCLDVNTELNSSIEDLLEASMSSTDTYTFKSEVAVLP-----1158  
Db 207 E-----TSQCMIDLPSAENSLSGSQSLDRSADSPSRKQMSVARSFPDRRECS 259  
QY 1159 -----EKAENDPY-----KDVNHNQCKEKEAEELALAI--AMMASAQ 1199  
Db 260 DRETQIDKGVKGTTPRRIRYVSHHKDYNDGKRTFFPIRHOGLNLTIVSSSLSTNG 319  
QY 1200 DALPITVPQ-----LOVENGEIIITQODTPETLPHTKAKOPYREDTEWLKGOQIGLG 1252  
Db 320 ENMGVAQYLDPRGLRSGADSENALVQERNVPT-----KSP--SAPIMNRCKLLGOG 371  
QY 1253 AFSSCYAQOVGCTLMAVQVTVYRNTSSQOEVEYVEALREIIMMSHLNPNITRMGA 1312  
Db 372 AFGVYTCYDVTDRRELASQVOFPDP--SPETSKEVSALBEIOLKNLOHERIYOYGC 430  
QY 1313 TCEKSN--YNLFEMMAGSVAHLISKYGAFKESVIVNTEOLLRGSLYHENQIHRD 1370  
Db 431 LRDAERKLTITFMEYMEGGSVKDQLKAYGALTESYTRKTYQLLEGMSYLSNMTIHRD 490  
QY 1371 KGANLLIDSTGQRLRIADFGAARLAS--KGTGAGEFOGOLLGTIAFMAPEVLRGOQY 1427  
Db 491 KGANILRDSAG--NVKLGDFGASKRLQITICMSGTGI--RSVTGTPYMWSPSEVTSIGEGY 545  
QY 1428 RSCQVWSYGCAIIEMACAKPPMAEKHSNHLALIFKIASATTAPSIPIHSLSGLDVALR 1487  
Db 546 RKADVWSJGCTVLEMPACKRPPW--AEYEA--MAAIFKATOPTNPOLPSHISEHGRDF--LR 601  
QY 1488 CLELOPQDRPPSRELLKH 1505  
Db 602 RIFVEARORPSAEELTH 619





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DQ      1477 LSPGLRDVALRCLCELODPDRPPRELLKH 1505
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Db      592 ISENGGRDF-LRRFLVEAKRPSSAEELLTH 619
DQ      535 SPEVISEGEGYGRADVWMSLCTGVDMLETKPEPW-AYEYA--MAAFKLTATQPTNTQLSH 591
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RESULT 13  
US-10-000-864-10

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Sequence 10, Application US/10000864
Patent No. US20020146798A1
GENERAL INFORMATION:
APPLICANT: CADUS PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: HUMAN MEK1 PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: CPT-0855CPC
CURRENT APPLICATION NUMBER: US/10/000,864
CURRENT FILING DATE: 2001-10-31
EARLIER APPLICATION NUMBER: 09/423,890
EARLIER FILING DATE: 2000-06-03
EARLIER APPLICATION NUMBER: PCT/US99/05556
EARLIER FILING DATE: 1999-03-15
EARLIER APPLICATION NUMBER: USSN 60/078,153
EARLIER FILING DATE: 1998-03-16
EARLIER APPLICATION NUMBER: USSN 60/099,165
EARLIER FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 619
TYPE: PRT
ORGANISM: Mus musculus
US-10-000-864-10

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Query Match 6.88; Score 531; DB 12; Length 619;  
Best Local Similarity 28.48; Pred. No. 4.8e-21;  
Matches 168; Conservative 78; Mismatches 214; Indels 132; Gaps 24;

QY	944	TTTTTTCOPRPMYQTGRPHSCLINSSPHSHSOLMFALPSTPSSSTPSPVAGTATDVK	1003
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QY	1004	H--RLOGFPCR-----IPASFPQGRKESLQFHRNCPENKSDKLSFVYQSRLEPSSN	1056
Db	176	QIARNGSFTSINSEGEFIPESMDQMDPLSTL-----SPSPSGSGSCPSTL-----DSPLODES	228
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Db	229	Y--PKSMP-----RAQSTPDNHQFTD--NPTEKKGKGTVPRRYHVSYHMQEYND	279
QY	1102	SNAPISDETVTPVEEKCRLDVNFTLANSIEDLLASMPSSDTPVTEKSEVAVLSPCKA	1161
Db	280	GKRTFP-----RARQTGTSFRSPV-----SPSPDHSLSHSSGSSVTPTE--	320
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QY	1222	DPEE-TLPGHTKAKOPYREDTEWLKQOIGLGAFFSCYOADVGCTLMAKOVYVYNT	1280
Db	334	DNPTLYTDSPPSRSPRAPPTNNRKLKLLGQAGFGAVIYCTYVDPTGRELAKQOYF-NPE	392
QY	1281	SSQEEVEVALREELRNMSHLNHPNIIIMLGATC-----EKSYNLFTEMMAGGSVAHLLS	1336
Db	393	SPESKSEVNALCEQIOLLNKLNLHERIVQYGG--CARDPQKTLSTIFMELSPGSGSTKQDK	450
QY	1337	KYGAFKFSYVINTTEOLLGLSTLHENQIHHVDVAGANLLIDSTQGRLLIRIDEGAAATA	1396
Db	451	AYGALTEWTRKTTROLCEVHLSNNMLVHVDIGKANLIRDSTQ--NKLIDPFGASKRLQ	509

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Db 565 EA-MAALFIATQTPINPKLPVSDYTDLF-LKRIFYAKRLRPSEAEELRH 613

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US-10-000-864-4  
; Sequence 4, Application US/10000864

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? Patent No. US20020146798A1
? GENERAL INFORMATION:
? APPLICANT: CADUS PHARMACEUTICAL CORPORATION
? TITLE OF INVENTION: HUMAN MEK1 PROTEIN AND NUCLEIC ACID MOLECULES
? TITLE OF INVENTION: AND USES THEREFOR
? FILE REFERENCE: CPT-085CPC
? CURRENT APPLICATION NUMBER: US/10/000,864
? CURRENT FILING DATE: 2001-10-31
? EARLIER APPLICATION NUMBER: 09/423,890
? EARLIER FILING DATE: 2000-06-03
? EARLIER APPLICATION NUMBER: PCT/US99/05556
? EARLIER FILING DATE: 1999-03-15
? EARLIER APPLICATION NUMBER: USSN 60/078,153
? EARLIER FILING DATE: 1998-03-16
? EARLIER APPLICATION NUMBER: USSN 60/099,165
? EARLIER FILING DATE: 1998-09-04
? NUMBER OF SEQ. ID NOS: 38
? SOFTWARE: PatentIn Ver. 2.0
? SEQ. ID NO. 4
? LENGTH: 619
? TYPE: PRT
? ORGANISM: Homo sapiens
? OS-10-000-864-4

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Query Match	6.8%	Score 530	DB 12	Length 619
Best Local Similarity	26.9%	Pred. No. 5.5e-21		
Matches 191; Conservative	90;	Mismatches 252;	Indels 176;	Gaps 32

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QY	920	LSASSEDISERLASISVGPSSSTTTT-----TTTEQPKPMVQTKR-----	961
Db	61	RPVKLEDLRSK-SKIFAGSQMDLHYNNELVPIPTQDDLDKAVELDLRSIHMSLKITLL	119
QY	962	-----PHASQNLNSPLSHSQLOMFRLSPRSSSTPVPACSTADVSKNHLQ	1007
Db	120	VWNGSTQAINLEPSPEDENNTNPGLAEKKKRLSVYGGPNNRDRSSPPPGYIPD-ELHOTA	178
QY	1008	---GFIPCR---IPASAPOTQRFKSLQFHNRCEKNKSDKLSLSEVFQSPRLESSNIHR	1059
Db	179	RNGSFTSINSEGEFIPESMDQMLDPLSL---SSPENSGSGSCP5L--DSDLDGESH--	229
QY	1060	PKRSRPFGTKSQGDPKSKNSMTLDLNSSKCKDDSGCCS-----NSSNA	1104
Db	230	PKSRMP-----RAQSPYPDHNOEFTDD--NP1FEKFGKGQTVPRRYHVSYHHOEXNGRK	282
QY	1105	V1RSDEVTFPVBEKCRLDVNTLELNSSIDLLEAAMPSSDTPVTEKSEVAVLSPKAEKD	1164
Db	283	TTF-----RARRRQGT5FSRPPV-----SFSPTDHL5LSSSSSVTFPE-----	320
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Job time : 29 secs

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OM protein - protein search, using sw model

Run on: December 20, 2002, 16:20:45 ; Search time 21 Seconds  
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2118.450 Million cell updates/sec

Title: US-09-697-898-2  
Perfect score: 7825  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6912.5	88.3	1493	4 US-09-423-890-8	Sequence 8, Appl1
2	6667	85.2	1593	4 US-08-628-829-4	Sequence 4, Appl1
3	6318.5	80.7	1302	4 US-09-423-890-2	Sequence 2, Appl1
4	3102.5	39.6	672	1 US-08-049-254-2	Sequence 2, Appl1
5	3102.5	39.6	672	1 US-08-472-934-2	Sequence 2, Appl1
6	3102.5	39.6	672	2 US-08-323-460A-2	Sequence 2, Appl1
7	3102.5	39.6	672	2 US-08-461-145C-2	Sequence 2, Appl1
8	3102.5	39.6	672	3 US-08-461-145C-2	Sequence 2, Appl1
9	3102.5	39.6	672	4 US-08-628-829-2	Sequence 2, Appl1
10	359	7.1	626	4 US-08-472-934-6	Sequence 6, Appl1
11	559	7.1	626	2 US-08-323-460A-6	Sequence 6, Appl1
12	559	7.1	626	2 US-08-461-145C-6	Sequence 6, Appl1
13	559	7.1	626	4 US-09-423-890-12	Sequence 12, Appl1
14	559	7.1	626	4 US-08-628-829-10	Sequence 10, Appl1
15	559	7.1	626	4 US-08-628-829-10	Sequence 12, Appl1
16	543	6.9	619	1 US-08-472-934-12	Sequence 12, Appl1
17	543	6.9	619	2 US-08-461-145C-12	Sequence 12, Appl1
18	543	6.9	619	3 US-08-461-145C-12	Sequence 12, Appl1
19	543	6.9	619	4 US-08-628-829-8	Sequence 8, Appl1
20	534.5	6.8	626	4 US-09-423-890-6	Sequence 6, Appl1
21	531	6.8	619	2 US-08-472-934-4	Sequence 4, Appl1
22	531	6.8	619	1 US-08-323-460A-4	Sequence 4, Appl1
23	531	6.8	619	2 US-08-461-145C-4	Sequence 4, Appl1
24	531	6.8	619	3 US-08-461-145C-4	Sequence 4, Appl1
25	531	6.8	619	4 US-09-423-890-10	Sequence 10, Appl1
26	531	6.8	619	4 US-08-628-829-6	Sequence 6, Appl1
27	530	6.8	619	4 US-09-423-890-4	Sequence 4, Appl1

28	478	6.1	1247	1 US-08-472-934-10	Sequence 10, Appl1
29	478	6.1	1247	2 US-08-323-460A-10	Sequence 10, Appl1
30	478	6.1	1247	2 US-08-461-145C-10	Sequence 10, Appl1
31	478	6.1	1247	3 US-08-461-145C-10	Sequence 10, Appl1
32	475	6.1	1597	4 US-09-423-890-13	Sequence 13, Appl1
33	475	6.1	1597	4 US-08-628-829-14	Sequence 14, Appl1
34	433	5.5	890	1 US-08-472-934-8	Sequence 8, Appl1
35	433	5.5	890	2 US-08-323-460A-8	Sequence 8, Appl1
36	433	5.5	890	2 US-08-461-145C-8	Sequence 8, Appl1
37	433	5.5	890	3 US-08-461-145C-8	Sequence 8, Appl1
38	433	5.5	890	4 US-08-628-829-12	Sequence 12, Appl1
39	427.5	5.5	1375	4 US-09-171-410-1	Sequence 1, Appl1
40	389.5	5.0	403	2 US-08-755-728-4	Sequence 1, Appl1
41	389.5	5.0	403	3 US-08-974-655-4	Sequence 4, Appl1
42	389.5	5.0	403	4 US-09-283-011-4	Sequence 4, Appl1
43	378.5	4.8	524	2 US-08-615-942A-2	Sequence 2, Appl1
44	376.5	4.8	545	2 US-08-935-760-4	Sequence 4, Appl1
45	374.5	4.8	544	2 US-08-935-760-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1  
US-09-423-890-8  
; Sequence 8, Application US/09423890  
; Patent No. 6312934  
; GENERAL INFORMATION:  
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION  
; TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES  
; FILE REFERENCE: CPI-085CPC  
; CURRENT APPLICATION NUMBER: US/09/423,890  
; CURRENT FILING DATE: 2000-03-06  
; PRIOR APPLICATION NUMBER: USSN 60/078,133  
; PRIOR FILING DATE: 1998-03-16  
; PRIOR APPLICATION NUMBER: USSN 60/099,165  
; PRIOR FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 1493  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-423-890-8

Query Match	88.3%	Score 6912.5;	DB 4;	Length 1493;
Best Local Similarity	89.5%	Pred. No. 0;		
Matches 1358;	Conservative 47;	Mismatches 82;	Indels 31;	Gaps 11;
QY 1	MAAAGNRASSSGPGARATSPEA---GGGGALKASGAPAA-AAAGLREAGSGGERAD	56		
DB 1	MAAAGNRASSSGPGARATSPEA---GGGGALKASGAPAA-AAAGLREAGSGGERAD	60		
QY 57	WRRHQLRRVSVELDQLEPQPLFL-ASPPASSTSPSPEDDAAGSGTGFPVAVPPHG	115		
DB 61	WRRHQLRRVSVELDQLEPQPLFL-ASPPASSTSPSPEDDAAGSGTGFPVAVPPHG	120		
QY 116	AASRGALHTSVAPDPSGASPPAAPERGERKRAAERSPAAAPAGRMEKKTILKGLHK	175		
DB 121	AASRGALHTSVAPDPSGASPPAAPERGERKRAAERSPAAAPAGRMEKKTILKGLHK	170		
QY 176	MDDPPEEMIEKTKATCMPMKHEMLERRNRGPVYVKPIPVKGDGSEMHLAESPGE	235		
DB 171	MDDPPEEMIEKTKATCMPMKHEMLERRNRGPVYVKPIPVKGDGSEMHLAESPGE	230		
QY 236	VQASAPASGASGSPSGNSPSGRIVKSESPPGVRRKRVSPVPOSGRTTPRRAPSPDG	295		
DB 231	VQASAPASGASGSPSGNSPSGRIVKSESPPGVRRKRVSPVPOSGRTTPRRAPSPDG	290		
QY 296	FSPTSPETSRKRVKVRARLYLLOQIGPNSFLIGDSDPKKRVVFVFGPQNSCARGTFC	355		
DB 291	FSPTSPETSRKRVKVRARLYLLOQIGPNSFLIGDSDPKKRVVFVFGPQNSCARGTFC	350		

Qy	366	IHFVWLVRYQLEPSPDMLWRTKLNKEFESIFOKYXHSRSSRIKAPBRNTIOKFVSM	415
Dd	331	IHLFVLMRYAQLEPSDPMMLWRTKLNKEFESLFOKXHSRSSRIKAPBRNTIOKFVSM	410
Qy	416	SNSHLTSSSTSTSSSENSIKDEEQOCPICLLGMLDEESLTVCEDGCKNKLHHHCMSIM	475
Dd	411	SNSHLTSSSTSTSSSENSIKDEEQOCPICLLGMLDEESLTVCEDGCKNKLHHHCMSIM	470
Qy	476	AEECRNRREPLICLCSKMSKSHDPFSHELSSVYDPSLSRAAOQOTVOOPLACS-RRN	534
Dd	471	AEECRNRREPLICLCSKMSKSHDPFSHELSSVYDPSLSRAAOQOTVOOPLACSORN	530
Qy	535	QESNFNLTHYGTQOIPAYKDLAEPMTIOVGMELVCLTESRMNVNEMALRLRSHDVSGA	594
Dd	531	QESSNLIHFTQOIPAYKDLAEPMTIOVGMELVCLTESRMNVNEMALRLRSHDVSGA	590
Qy	595	LLLANGESTGNSGGSGSSPBGATSGSSQTSISGDVEACSSVLSMWCADPVYKYYAA	654
Dd	591	LLLANGESTGNSGGSGSGSLSAGASGSSOPSISGDVEACSSVLSIYCADPVYKYYAA	650
Qy	655	LKTLRAMVYVPPCHSLAEIRIKLRILOPVYDTLVYCAANSTQSLSTLLELCKGGA	714
Dd	651	LKTLRAMVYVPPCHSLAEIRIKLRILOPVYDTLVYCAANSTQSLSTLLELCKGGA	710
Qy	715	GELAVGREILKAGSIGIGVDYVNLCTILIGNOTESNMWOELLGRLCIDLLEFPAAEFP	774
Dd	711	GELAVGREILKAGSIGIGVDYVNLCTILIGNOTESNMWOELLGRLCIDLLEFPAAEFP	770
Qy	775	HYVSDVSOAPVPIRIRKRLLSLTLFALOSINDSHSNMGLSRITLSARAWTYVPAVF	834
Dd	771	HYVSDVSOAPVPIRIRKRLLSLTLFALOSINDSHSNMGLSRITLSARAWTYVPAVF	830
Qy	835	SKLEMLSVSSSTFTFTMMRRRLMAIADEVIAEAIOLGVEDTLDCQODSFLOASVPNNLT	894
Dd	831	SKLYTMLNASSSTFTFTMMRRRLMAIADEVIAEAIOLGVEDTYDGHQDS-LQAVAPSTGL	889
Qy	895	ETTEHNSPECTVHLKTKGKLCATKLSASSEDISERLASSVGPSSSTTTTTTTEBQKP	954
Dd	890	---ENSSLEHNVHNEKKGKLSATRLSASSEDISDRLAGSVGLPSS---TTTEBQKP	941
Qy	955	MYOFKGRHSOCLNPSFLSHSOLMFPALTPSSSPVPAQATDVSXKRLROGFPICI	1011
Dd	942	AVOIKGRHSOCLNPSFLS-HAOLMFPABAPCSSAPVP-----DISHNRQATVPCKI	995
Qy	1015	PSASPOQORFSLQFHNRCEPNKDKLSFVQOSRPLPSSNIIHRKPSRPTPGNTSKOG	1074
Dd	996	PSASPOQORFSLQFQRNCCSEHRSDQLSPVFIQSRPPSSNIIHRKPSRPVPGNTSKLG	1055
Qy	1075	DPKNSMNTLDNSSKCDSDSGGSSNSNNAVITPSDETFTVPBEKRLDYNTMELNSSIED	1133
Dd	1056	DATSSMNTLDLGSASKCDSDSGGSGNSGNNAVITPSDETFTVPBECKRLDYNTMELNSSIED	1115
Qy	1135	LLEASMPSSDITVFKSEEVAVLSPERKANDDYTKDDVNNHNOCKKEMEAEEEBEALAIAMA	1194
Dd	1116	LLEASMPSSDITVFKSEEVAVLSPERKANDDYTKDDVNNHNOCKKEMEAEEEBEALAIAMA	1177
Qy	1195	MSASODALPIVPOLOVENGEDIIITOODPTEPLPGHTKAKOPYREDTEMLKCOQIGLGAF	1255
Dd	1176	MSASODALPIVPOLOVENGEDIIITOODPTEPLPGHTKAKOPYREDAEWMLKCOQIGLGAF	1233
Qy	1255	SSCVOADOVGTGLMAVKQTYVYANTSSEBEEVVALREIRIMSHLNPNTIIRMLGATC	1314
Dd	1236	SSCVOADOVGTGLMAVKQTYVYANTSSEBEEVVALREIRIMSHLNPNTIIRMLGATC	1299
Qy	1315	EKSNNYLFIEWMAGSVAHLLSKYGAFKESVINTYEDOLLRGLSYLHENQOIIHRDVKGAN	1374
Dd	1296	EKSNNYLFIEWMAGSVAHLLSKYGAFKESVINTYEDOLLRGLSYLHENQOIIHRDVKGAN	1355
Qy	1375	LLIDSTQORLRIADFGAARLASKGTGAGFGOQLLGTLTAFNAPRYVLRCOOYGRSCDWJS	1433
Dd	1356	LLIDSTQORLRIADFGAARLASKGTGAGFGOQLLGTLTAFNAPRYVLRCOOYGRSCDWJS	1415

QY	1435	VGCATIEAACAKPMPNNAKSHNHLALFKIKASATPASPISHLSPGLDVALRCLELQPO	1494
DB	1416	VGCATIEAACAKPMPNNAKSHNHLALFKIKASATPASPISHLSPGLDVALRCLELQPO	1475
QY	1495	DRPPSRELLKHVFERTTW	1512
DB	1476	DRPPSRELLKHVFERTTW	1493
RESULT 2			
US-08-628-829-4			
: Sequence 4, Application US/08628829A			
: Patent No. 6333170			
: GENERAL INFORMATION:			
: APPLICANT: Johnson, Gary L.			
: TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To External			
: FILE REFERENCE: Cpl-004DVCp3			
: CURRENT APPLICATION NUMBER: US/08/628, 829A			
: CURRENT FILING DATE: 1996-04-05			
: EARLIER APPLICATION NUMBER: 08/440,421			
: EARLIER FILING DATE: 1995-05-15			
: EARLIER APPLICATION NUMBER: 08/323,460			
: EARLIER FILING DATE: 1994-10-14			
: EARLIER APPLICATION NUMBER: 08/049,254			
: EARLIER FILING DATE: 1993-05-15			
: EARLIER APPLICATION NUMBER: 08/410,602			
: EARLIER FILING DATE: 1995-04-24			
: EARLIER APPLICATION NUMBER: 08/472,934			
: EARLIER FILING DATE: 1995-06-06			
: NUMBER OF SEQ ID NOS: 25			
: SOFTWARE: PatentIn Ver. 2.0			
: SEQ ID NO 4			
: LENGTH: 1593			
: TYPE: PRT			
: ORGANISM: Mus musculus			
US-08-628-829-4			
Query Match			
Best Local Similarity 85.2%; Score 6667; DB 4; Length 1593;			
Matches 1322; Conservative 49; Mismatches 102; Indels 58; Gaps 13;			
QY	1	MAAAGNRASSGGFPGARATSPEA---GGGGALTKASSAPAA-AGLLIREAGSGGERAD	56
DB	102	MAAAGDRASSGGFPGAAASPEAGGGGGGALDGGCAPAAGALLREPGASPART	161
QY	57	-----WRRQLKRVSVLELDQLPEQPLFLAASPPASSTSPSEPADAAGSGTGF	105
DB	162	GGGGTCACGWSWTSICSSRS-----SSPPRRPAHLPLVAGARGCGRS	207
QY	106	QPV---AVPPHGAASRGGAHLTESVAAPDGSASPAAAFGEKRAAPAPSPAAAPAGR	162
DB	208	ESLPRAAGPPPPGAASRCGSHSAELAAARADGARGPAAEP-----PS-AAAPSGR	257
QY	163	EENENETLGLKHMDDREERMIREKTKATCMPANKHEMLEERNRNGPVVVKPIPVKDG	222
DB	258	EENENETLGLKHMDDREERMIREKTKATCMPANKHEMLEERNRNGPVVVKPIPVKDG	317
QY	223	SEMNLAAESQEVQASAPSPASKGRSPSPQNSFGTGVVASESGVRRKRVYPVPOSG	282
DB	318	SEVNNLAAEPQEGGAAPAPKGRSPSPGSSPSGRSVKPESGVRRKRVYPVPOSG	377
QY	283	RTPPRRAAPSPDGFSPYSPPEETNRVRNKKVMARALYLLQIGNSPFLIGDSPDNKYRFT	342
DB	378	RTPPRRAAPSPDGFSPYSPPEETNRVRNKKVMARALYLLQIGNSPFLIGDSPDNKYRFT	437
QY	343	GPONSCARGTCFTHLFLVMLRVFQLEPSDPLMTKTLKNEVESLFFOKYHSRRSRITKA	402
DB	438	GPONSCARGAFCIHLFLVMLRVFQLEPSDPLMTKTLKNEVESLFFOKYHSRRSRITKA	497
QY	403	PSRNTIQFVSRMSNHLSSSTSTSSSENSIKDEEQMCPICLLGLMLDEBSLTVLEDG	462
DB	498	PSRNTIQFVSRMSNHLSSSTSTSSSENSIKDEEQMCPICLLGLMLDEBSLTVLEDG	557





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Db 661 LMAIADEVEIAEVIQIGVEDIYDGHODS--LQALAPASCL---ENSSLEHTVHREKTKGCL 716
Qy 916 CATKLSASSEDISERLASISVGPSSSTTTTTEQPKPMVQTKGRPHSQCINSSPLSHR 975
Db 717 SATRLSASSEDISDRLAGVSGVLPSS-----TTTEQPKPAVQTKGRPHSQCINSSPLS-H 770
Qy 976 SOLMPALSTPSSSPSVAGTATDYSKHLQGFICRIPASAPQORFSLQFHNCPRE 1035
Db 771 AQLMFPAPSPASAPSV-----DISKHPQAFVPCKIPASAPQORFSLQFHNCPRE 825
Qy 1036 NKDSKLSVFTQSRPLPSSNIHRPKSRPTPGNTSKQDPSKNSMTLDLNSSKCDPSF 1095
Db 826 HBDSDQLSVFQSRPSPSSNIHRPKSRPVPGSTSKLGDATKSMSTLDLGSRCDDSF 885
Qy 1096 GCSNSSNAVIDSDEFTVTPVECKRLDVNTEINSSIEDLLEASMPSSDTTTFKSEVAV 1155
Db 886 GGGGNGSNVIPSDEFTVTPVECKRLDVNTEINSSIEDLLEASMPSSDTTTFKSEVAV 945
Qy 1156 LSPKENDDTYKDDVNNHOKCKEKEAEEREAALAMAMASQDALPIYPOQVENGED 1215
Db 946 LSPKENDDTYKDDVNNHOKCKEKEAEEREAALAMAMASQDALPIYPOQVENGED 1005
Qy 1216 IITIQDTEETLPGHTKAKOPYREDEWEMLKGOQIGLAFSSCYQADVGITLMAVKQYT 1275
Db 1006 IITIQDTEETLPGHTKAKOPYREDEWEMLKGOQIGLAFSSCYQADVGITLMAVKQYT 1065
Qy 1276 YVRNTSSEDEVEEVALREIRMMSHLNHPNIRMLGATCEKSNYNLFIEEMAGSVAHLL 1335
Db 1066 YVRNTSSEDEVEEVALREIRMMSHLNHPNIRMLGATCEKSNYNLFIEEMAGSVAHLL 1125
Qy 1336 SKYGAKESVINYTPQRLRGISYLHENQIHRDVGANLLIDSTQORLIADFGAAARL 1395
Db 1126 SKYGAKESVINYTPQRLRGISYLHENQIHRDVGANLLIDSTQORLIADFGAAARL 1185
Qy 1396 ASKGTCAGEFQGLGTIAFMAPEVLRGQOYGRSCDWSVGCALIIEMACAKPPWNAEKHS 1455
Db 1186 ASKGTCAGEFQGLGTIAFMAPEVLRGQOYGRSCDWSVGCALIIEMACAKPPWNAEKHS 1245
Qy 1456 NHALIFKIASATTAPISHSISGLRDVALRCLLEQPODRPPSRRLKHVPFRITW 1512
Db 1246 NHALIFKIASATTAPISHSISGLRDVALRCLLEQPODRPPSRRLKHVPFRITW 1302

RESULT 4
US-08-049-254-2
; Sequence 2, Application US/08049254
; Patent No. 5405941
; GENERAL INFORMATION:
; APPLICANT: Johnson Ph.D., Gary L.
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
; TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH, P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,254
; FILING DATE: 19930415
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik Esq., Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-1
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; TELEX: 467317
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 672 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-049-254-2

Query Match      39.6%; Score 3102.5; DB 1; Length 672;
Best Local Similarity 89.2%; Pred. No. 66-194;
Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

Qy 826 MTTTTPHVSFKLEMLSVSSSTHTFRMRRLMAIAEVEIAEVIQIGVEDIYDGHODSFL 885
Db 1 MTTTTPHVSFKLEMLSVSSSTHTFRMRRLMAIAEVEIAEVIQIGVEDIYDGHODS-L 59
Qy 886 QASVPMNNYLETTEENSSPECTVHLEKTKGICATKLSASSEDISERLASISVGPSSSTTTT 945
Db 60 QAVAPTSCL---ENSSLEHTVHREKTKGISATRLSASSEDISDRLAGVSGVLPSS----- 112
Qy 946 TTTTEQPKPMVQTKGRPHSQCINSSPLSHSOLMFPALSTPSSSTPSVAGTATDYSKHLR 1005
Db 113 -TTTEQPKPAVQTKGRPHSQCINSSPLS-HAQLMFPAPSPASAPSV-----DISKHR 165
Qy 1006 LQGFICRIPASAPQORFSLQFHNCPENKDSKLSVFTQSRPLPSSNIHRPKSRP 1065
Db 166 PQAFVPCKIPASAPQORFSLQFHNCPENKDSKLSVFTQSRPSPSSNIHRPKSRP 225
Qy 1066 TPGNTSKQDPSKNSMTLDLNSSKCDPSFSGCSNSSNAVIDSDEFTVTPVECKRLDVN 1125
Db 226 VPGSTSKLGDATKSMSTLDLGSASRCDDSFSGGNGSNVIPSDEFTVTPVECKRLDVN 285
Qy 1126 TELNSSIEDLLEASMPSSDTTTFKSEVAVLSPKENDDTYKDDVNNHOKCKEKEAEER 1185
Db 286 TELNSSIEDLLEASMPSSDTTTFKSEVAVLSPKENDDTYKDDVNNHOKCKEKEAEER 345
Qy 1186 EEAALAMAMASQDALPIYPOQVENGEDIIITQDTEETLPGHTKAKOPYREDEWEMLK 1245
Db 346 EEAALAMAMASQDALPIYPOQVENGEDIIITQDTEETLPGHTKAKOPYREDEWEMLK 405
Qy 1246 GQOIGLAFSSCYQADVGITLMAVKQYTYVRNTSSEDEVEEVALREIRMMSHLNHPN 1305
Db 406 GQOIGLAFSSCYQADVGITLMAVKQYTYVRNTSSEDEVEEVALREIRMMSHLNHPN 465
Qy 1306 IIRMLGATCEKSNYNLFIEEMAGSVAHLLSKYGAKESVINYTPQRLRGISYLHENQI 1365
Db 466 IIRMLGATCEKSNYNLFIEEMAGSVAHLLSKYGAKESVINYTPQRLRGISYLHENQI 525
Qy 1366 IHRDVGANLLIDSTQORLIADFGAAARLASKTGAGEFQGLGTIAFMAPEVLRGQO 1425
Db 526 IHRDVGANLLIDSTQORLIADFGAAARLASKTGAGEFQGLGTIAFMAPEVLRGQO 585
Qy 1426 YGRSCDWSVGCALIIEMACAKPPWNAEKHSNHALIFKIASATTAPISHSISGLRDVA 1485
Db 586 YGRSCDWSVGCALIIEMACAKPPWNAEKHSNHALIFKIASATTAPISHSISGLRDVA 645
Qy 1486 LRCLLEQPODRPPSRRLKHVPFRITW 1512
Db 646 VRCLLEQPODRPPSRRLKHVPFRITW 672

RESULT 5
US-08-472-934-2
; Sequence 2, Application US/08472934
; Patent No. 5753446
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, GARY L.
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
; TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
; NUMBER OF SEQUENCES: 12

```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lahive and Cockfield  
;; STREET: 60 State Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: U.S.A.  
;; ZIP: 02109  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentln Release #1.0, Version #1.25  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/472,934  
;; FILING DATE: 06-JUN-1995  
;; CLASSIFICATION: 435  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/440,421  
;; FILING DATE: 15-May-1995  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/354,516  
;; FILING DATE: 21-FEB-1995  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 5,405,941  
;; FILING DATE: 15-Apr-1993  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/323,460  
;; FILING DATE: 14-Oct-1994  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US94/11690  
;; FILING DATE: 14-Oct-1994  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US94/04178  
;; FILING DATE: 15-APR-1994  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Giulio A. Decontii, Jr. Esq.  
;; REGISTRATION NUMBER: 31,503  
;; REFERENCE/DOCKET NUMBER: CPT-004DVCPE2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 227-7400  
;; TELEFAX: (617) 227-5941  
;;  
;; INFORMATION FOR SEQ. ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 672 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-472-934-2

Query Match 39.6%; Score 3102.5; DB 1; Length 672;  
Best Local Similarity 89.2%; Pred. No. 6e-194;  
Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

QY 826 MATTVAHVFSKLEMLSVSSSTHFTRRRLMAIADEVETAEIAIQGVEDTLTGQDSFL 885  
DB 1 MTTVAHVAVSVSKLTMTLNASSSTHFTRRRLMAIADEVETAEIAIQGVEDTLTGQDS- 59  
QY 886 QASVPMNYLETTESSSPECTVHLEKTKGKCATKRLSASSEDISPRLASISVGPSSSTTTT 945  
DB 60 QAVAPTSCL---ENSSLEHTVHREKTKGKLSATRLSASSSEDISRLAGVSGLPSS---- 112  
QY 946 TTTTEOPKPVWQTKGRHSCCLNSSPLSHSOLMFPALSTPSSSTPSVPAQTADVSKHR 1005  
DB 113 -TTTEOPKPAVQTKGRHSCCLNSSPLS-HAQLMFPAPAPSCSAPSV-----DISK 165  
QY 1006 LOGFIFCRITISASPOQORAKSLQFHRKCPKNSKSDKSLPVFTQSRPLPSSNIHRPKSRP 1065  
DB 166 PQAFVFPCKIPSPQORAKSLQFHRKCPKNSKSDKSLPVFTQSRPLPSSNIHRPKSRP 225  
QY 1066 TPENTSKQDPSKNSMTLDLNSSSKCDSPGCSNNSNAVIPSDEYVFTVEEKCRLDVN 1125  
DB 226 VPSTSKLGDATKSSMTLDLGSASRCDDSRGGGSGNSGNAVIPSDEYVFTVEEKCRLDVN 285

QY 1126 TELNSSIEDILLEASMPSSDTTTFKSEVAVALSPEKAENDTYKDDVNHNOCKEKEAE 1185  
DB 286 TELNSSIEDILLEASMPSSDTTTFKSEVAVALSPEKAENDTYKDDVNHNOCKEKEAE 345  
QY 1186 EELATAMAMASODALPIYPOQLQVENGEDIIIIQDPTPLGHTAKQPYREDTBLK 1245  
DB 346 EELATAMAMASODALPIYPOQLQVENGEDIIIIQDPTPLGHTAKQPYREDTBLK 405  
QY 1246 GQOIGLGFSSCYOAOQDVGTGLMAVKQYVYRNTSSQEEVEALREIRMSHLNHPN 1305  
DB 406 GQOIGLGFSSCYOAOQDVGTGLMAVKQYVYRNTSSQEEVEALREIRMSHLNHPN 465  
QY 1306 IIRMLGATCKESVNYLFIEMAGGSVAHLISKYGAFFESVYINTEQLLGLSYLHENQ 1365  
DB 466 IIRMLGATCKESVNYLFIEMAGGSVAHLISKYGAFFESVYINTEQLLGLSYLHENQ 525  
QY 1366 IHRDVGANLLIDSTGRLTIADFGAARLASKGTGGEFQGLGTIARMAPEVLRGQO 1425  
DB 526 IHRDVGANLLIDSTGRLTIADFGAARLASKGTGGEFQGLGTIARMAPEVLRGQO 585  
QY 1426 YGRSCDVWSVCATIEMACAKPPMAEKHSNHLALIKRIASATTAPISPSHLSPLGRDVA 1485  
DB 586 YGRSCDVWSVCATIEMACAKPPMAEKHSNHLALIKRIASATTAPISPSHLSPLGRDVA 645  
QY 1486 LRCLLELOPQDRPPSRELLKHVFRTTW 1512  
DB 646 VRCLLELOPQDRPPSRELLKHVFRTTW 672

RESULT 6  
US-08-323-460A-2  
Sequence 2, Application US/08323460A  
Patent No. 5854043  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, GARY L.  
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL  
TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SHERIDAN ROSS & MCINTOSH  
STREET: 1700 LINCOLN STREET, SUITE 3500  
CITY: DENVER  
STATE: CO  
COUNTRY: USA  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/323,460A  
FILING DATE: 14-OCT-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/049,254  
FILING DATE: 14-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOVARIK, JOSEPH E.  
REGISTRATION NUMBER: 33,005  
REFERENCE/DOCKET NUMBER: 2879-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/863-9700  
TELEFAX: 303/863-0223  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 672 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-323-460A-2

Query Match 39.6%; Score 3102.5; DB 2; Length 672;

Best Local Similarity 89.2%; Pred. No. 66-194;  
Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

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OY 826 MVTVPVHVSKELEMLSVSSSTHFTMRRLMAIADEVEIAEIQGVEDTLDGQDSFL 885
DB 1 MVTAVPAVSKLVMTMNASGTHFTMRRLMAIADEVEIAEIQGVEDTLDGQDS-L 59
OY 886 QASVPRNLYETENSSPECTVHLEKTKGLCATKLSASSEDISERLASISVGPSSSTTTT 945
DB 60 QAVAPISCL---ENSLFHTVREKTKGLSATRLSASSEDISDRLAGVSVGLPSS---- 112
OY 946 TTTTEOPKPMVOTKGRPHSQCLNSPLSHNSOLMPALSTPSSSTPSVAGTATDVSKHR 1005
DB 113 -TTTTEOPKPMVOTKGRPHSQCLNSPLS-HAOLMPAPAPCSAPSV-----DISKR 165
OY 1006 LOGFIPCRIPASPTQRFSLQFHRNCPENKDSKLSFVFTQSRPLPSSNTHRPKPSRP 1065
DB 166 PQAFVPCIKPSASPTQRFSLQFHRNCPENKDSKLSFVFTQSRPLPSSNTHRPKPSRP 225
OY 1066 TPGNNTSKODPSPKNSMTLDLNSKCDSDSPGSSNSNNAVIPSDEVPFVPEKCKLDVN 1125
DB 226 VPGSTSKLDATKSSMTLDLGSASRCDDSPGGGNSGNNAVIPSDEVPFVPEKCKLDVN 285
OY 1126 TELNSSIEDLEASMPSSDTVTYTFKSEVAVLSPEKAENDDTYKDDVNHNOCKEKEKAE 1185
DB 286 TELNSSIEDLEASMPSSDTVTYTFKSEVAVLSPEKAENDDTYKDDVNHNOCKEKEKAE 345
OY 1186 EELALAIAMAMASODALPIVPOLOVENGEDIIIOODTPELPGHTKAKOPYREDETWL 1245
DB 346 EELALAIAMAMASODALPIVPOLOVENGEDIIIOODTPELPGHTKAKOPYREDETWL 405
OY 1246 GOOIGGAFSSCYQADVGTGLMAVKQTYVRNNTSSDEEVEVLAEREIRMSHNLNHN 1305
DB 406 GOOIGGAFSSCYQADVGTGLMAVKQTYVRNNTSSDEEVEVLAEREIRMSHNLNHN 465
OY 1306 IIRMLGATCEKSNYLFIEFMAGGSVAHLSTKYGAFKESVINTYBOLLRGSLYHENOI 1365
DB 466 IIRMLGATCEKSNYLFIEFMAGGSVAHLSTKYGAFKESVINTYBOLLRGSLYHENOI 525
OY 1366 IIRDYKGANLLIDSTGOQLRIADFGAARLASKGTGAGEFQQLGTTAFMAPEVLRGOO 1425
DB 526 IIRDYKGANLLIDSTGOQLRIADFGAARLASKGTGAGEFQQLGTTAFMAPEVLRGOO 585
OY 1426 YGRSDVMSVGCATTEMACAPPMNAEKSHNLALIFKASNTATPASTISHLSPGLRDVA 1485
DB 586 YGRSDVMSVGCATTEMACAPPMNAEKSHNLALIFKASNTATPASTISHLSPGLRDVA 645
OY 1486 IIRLELOPQDRPSPRELKHPVFRTTW 1512
DB 646 IIRLELOPQDRPSPRELKHPVFRTTW 672

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RESULT 7  
US-08-461-146C-2  
Sequence 2, Application US/08461146C  
Patent No. 5981265

GENERAL INFORMATION:

APPLICANT: JOHNSON, GARY L.  
TITLE OF INVENTION: METHODS FOR REGULATING MEK PROTEIN ACTIVITY  
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lohive and Cockfield

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/461,146C
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/354,516
FILING DATE: 21-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 15-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,460
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CFI-004CN3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 672 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-146C-2

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Query Match 39.6%; Score 3102.5; DB 2; Length 672;

Best Local Similarity 89.2%; Pred. No. 66-194;  
Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

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OY 826 MVTVPVHVSKELEMLSVSSSTHFTMRRLMAIADEVEIAEIQGVEDTLDGQDSFL 885
DB 1 MVTAVPAVSKLVMTMNASGTHFTMRRLMAIADEVEIAEIQGVEDTLDGQDS-L 59
OY 886 QASVPRNLYETENSSPECTVHLEKTKGLCATKLSASSEDISERLASISVGPSSSTTTT 945
DB 60 QAVAPISCL---ENSLFHTVREKTKGLSATRLSASSEDISDRLAGVSVGLPSS---- 112
OY 946 TTTTEOPKPMVOTKGRPHSQCLNSPLSHNSOLMPALSTPSSSTPSVAGTATDVSKHR 1005
DB 113 -TTTTEOPKPMVOTKGRPHSQCLNSPLS-HAOLMPAPAPCSAPSV-----DISKR 165
OY 1006 LOGFIPCRIPASPTQRFSLQFHRNCPENKDSKLSFVFTQSRPLPSSNTHRPKPSRP 1065
DB 166 PQAFVPCIKPSASPTQRFSLQFHRNCPENKDSKLSFVFTQSRPLPSSNTHRPKPSRP 225
OY 1066 TPGNNTSKODPSPKNSMTLDLNSKCDSDSPGSSNSNNAVIPSDEVPFVPEKCKLDVN 1125
DB 226 VPGSTSKLDATKSSMTLDLGSASRCDDSPGGGNSGNNAVIPSDEVPFVPEKCKLDVN 285
OY 1126 TELNSSIEDLEASMPSSDTVTYTFKSEVAVLSPEKAENDDTYKDDVNHNOCKEKEKAE 1185
DB 286 TELNSSIEDLEASMPSSDTVTYTFKSEVAVLSPEKAENDDTYKDDVNHNOCKEKEKAE 345
OY 1186 EELALAIAMAMASODALPIVPOLOVENGEDIIIOODTPELPGHTKAKOPYREDETWL 1245
DB 346 EELALAIAMAMASODALPIVPOLOVENGEDIIIOODTPELPGHTKAKOPYREDETWL 405
OY 1246 GOOIGGAFSSCYQADVGTGLMAVKQTYVRNNTSSDEEVEVLAEREIRMSHNLNHN 1305
DB 406 GOOIGGAFSSCYQADVGTGLMAVKQTYVRNNTSSDEEVEVLAEREIRMSHNLNHN 465
OY 1306 IIRMLGATCEKSNYLFIEFMAGGSVAHLSTKYGAFKESVINTYBOLLRGSLYHENOI 1365
DB 466 IIRMLGATCEKSNYLFIEFMAGGSVAHLSTKYGAFKESVINTYBOLLRGSLYHENOI 525

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DB 491 KGANILDSAG-NVKLDFGASKRLQITCMSTGI-----RSVTGTPYMSPEVYSGGYG 545  
QY 1428 RSCDVMSVGCALIIEMACAKPPMNAEKHSNHLALIFKIASATTAPISPSHSPGLRDVALR 1487  
DB 546 RKADVMSIGCTVEMLEKPPW-AEYEA--MAAIFKATQPTNPQLPSHISEGRDE-LR 601  
QY 1488 CLELOPDRPPSRELLKH 1505  
DB 602 RIFVEARQPSAEELLTH 619  
RESULT 11  
US-08-323-460A-6  
Sequence 6, Application US/08323460A  
Patent No. 5854043  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, GARY L.  
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL  
RESPONSE TO EXTERNAL SIGNALS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SHERIDAN ROSS & MCINTOSH  
STREET: 1700 LINCOLN STREET, SUITE 3500  
CITY: DENVER  
STATE: CO  
COUNTRY: USA  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/323,460A  
FILING DATE: 14-OCT-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/049,254  
FILING DATE: 14-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOVARIK, JOSEPH E.  
REGISTRATION NUMBER: 33,005  
REFERENCE/DOCKET NUMBER: 2879-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/863-9700  
TELEFAX: 303/863-0223  
INFORMATION FOR SEQ. ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 626 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-323-460A-6  
Query Match 7.18; Score 559; DB 2; Length 626;  
Best Local Similarity 29.9%; Pred. No. 1.8e-28;  
Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;  
QY 1016 SASPOTORRKSIFGHRMCPENKSDKISPYETOSRPLPSN-----IHRPK----- 1062  
DB 110 SSMKSLRILLISODRA---HTSSPSHSGVSKOVRIRPSOSAGDINTIYQAPERSRHL 166  
QY 1063 -----SRPTG-----NTSKQDPKSNMTLIDJNSSKCDSDGSSNSNNAVIR 1107  
DB 167 VSSQNPGRSPPPGYVERQOHIAQO-----SYT-----SINSEGFIP 206  
QY 1108 SDEIVFPVEKRLDVNTELSIEDLLKSNMPSDTPVTFKSEVAVLSP----- 1158  
DB 207 E-----TSQCMIDPLTSAENSLSGSCSLDRSADSPSFRKSOEMRASFDPNRRECS 259  
QY 1159 -----EKAENDTY-----KDVNHNOKCKREKMEAEELALAI---AAMASQ 1199

DB 260 DREQLYDKGVGGTYRRRVHVSVHHKDYNDGRTPPRIRRHQGNLFTLYPSSRLSTNG 319  
QY 1200 DALPIVPO-----LOVENGEDIIIIQODTPETLPGRHAKOPYREDTEMLKGOQIGL 1252  
DB 320 ENMGVAQYIDLPRLRLSADSENALTYQERNVPT-----KSP-SAPIMMRBCKLLGOG 371  
QY 1253 AFSSCYQADYVGTCTLMAVKQVTVYRNTSSQEEVVALREIRBMWHLNPNIRMLGA 1312  
DB 372 AFRVYLYCYVDVDTGERELASKOVOPDP-SPEYSKREVALCEIOLLNKHRIYQYCC 430  
QY 1313 TCESN--VNFETEMAGSVAHLLSKYGAFKESVAVINTYEQLLRGISYHENQIIIRDY 1370  
DB 431 LRDRAEKILTEMETMFGSVKQDLKAYGALTESVTRKTYKOLLEGMSYLSHNMVHRDI 490  
QY 1371 KGANILDSGTQRLRIADFGAARLAS---KGTGAGEFOGLGTFIAPMAPEVLRGOQYG 1427  
DB 491 KGANILDSAG-NVKLDFGASKRLQITCMSTGI-----RSVTGTPYMSPEVYSGGYG 545  
QY 1428 RSCDVMSVGCALIIEMACAKPPMNAEKHSNHLALIFKIASATTAPISPSHSPGLRDVALR 1487  
DB 546 RKADVMSIGCTVEMLEKPPW-AEYEA--MAAIFKATQPTNPQLPSHISEGRDE-LR 601  
QY 1488 CLELOPDRPPSRELLKH 1505  
DB 602 RIFVEARQPSAEELLTH 619  
RESULT 12  
US-08-461-146C-6  
Sequence 6, Application US/08461146C  
Patent No. 5981265  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, GARY L.  
TITLE OF INVENTION: METHODS FOR REGULATING MEK PROTEIN ACTIVITY  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lahive and Cockfield  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,146C  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/354,516  
FILING DATE: 21-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/049,254  
FILING DATE: 15-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/323,460  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/11690  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04178  
FILING DATE: 15-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KARA, Catherine J.  
REGISTRATION NUMBER: P41,106  
REFERENCE/DOCKET NUMBER: CPI-00ACN3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 626 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-461-146C-6

Query Match 7.1%; Score 559; DB 2; Length 626;  
 Best Local Similarity 29.9%; Pred. No. 1.8e-28;  
 Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;

QY 1016 SASPQQRKFSLOFHRCNCEKNDKSLSPVFTQSRPLPSN-----IHRKP----- 1062  
 DB 110 SSSMKSLRILLLSQDRN---HTSSPHSGVSRQVRIRKPSQAGDINTITYQAPRGRHLS 166  
 QY 1063 -----SRPTPG-----NTSKQGDPSKSNMTLDLSSKCDSDFFCCSSNSSNAVIP 1107  
 DB 167 VSSQNGRSPSPGYPYPERQOHAROG-----SYT-----SINSEGEFTIP 206  
 QY 1108 SDEVTFTPEEKCRLDVNTLNSIEDLLEASMPSSDTVTYFKSEYAVLSP----- 1158  
 DB 207 E-----TSEQCMDPLPSAENSLSGSCSLDRSADSPSFRKSQMSRARSPDNKECS 259  
 QY 1159 -----EKAENDDY-----KDVYNNQCKEKEAEDEEALAI---AMAMASQ 1199  
 DB 260 DRETQLYDKGVKGTYPRRYHVSVHHKDYNDGRRTPPIRRHOGNLFLLVPSRSLSSTNG 319  
 QY 1200 DALPIYPO-----LQVNGEDIITIQDTPETLPGHTRAKOPYREDETEMLKGOQIG 1252  
 DB 320 ENMGVAVOYLDPRGRRLRSADSENALTVOERNPT-----KSP-SAPINMRGKLLGG 371  
 QY 1253 AFSSCYQADVGSTGLMAVKQYTYVNTSSQEEVEVALREIRMSHNLHNPITRMIGA 1312  
 DB 372 AGRVYLYCDVDTGRGLRSADSENALTVOERNPT-----KSP-SAPINMRGKLLGG 430  
 QY 1313 TCEKSN--YNLFTEWMASSVAHLISKYGAFFKESVINTTEQLRLSLYHENOITIRDY 1370  
 DB 431 LRDRAEKILITFMEYVPGSVKQDLKAYGALTESYRKYTRQILEKMSYLHSMYIHRDI 490  
 QY 1371 KGANLIDSTGORLRADGAARLAS---KGTAGEFQGLIGTATAPAPRYLKGQOYG 1427  
 DB 491 KGANILRDSAG-NVYKGDGASKRIOTICMSGTGI-----RSYTGTPYMWSPVISSEGG 545  
 QY 1428 RSCDVWSVCALITEMACAPPMNAEKSHNLALIFRIASATTAAPSISHLSPGLRDVALR 1487  
 DB 546 RADVWSLGCITYVEMLTEKPPM-AEYEA--MAAIFRIATOPTNPOLPSHISEGRDF-LR 601  
 QY 1488 CLELPODRPSPRELK 1505  
 DB 602 RIFVEAKORPSAEELLTH 619

RESULT 13  
 US-08-461-145C-6  
 ; Sequence 6, Application US/08461145C  
 ; Patent No. 6074861  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JOHNSON, GARY L.  
 ; TITLE OF INVENTION: NOVEL MEK PROTEINS  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lahnive and Cockfield, LLP  
 ; STREET: 60 State Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: U.S.A.  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/461,145C  
 ; FILING DATE: 5-JUNE-1995  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/049,254  
 ; FILING DATE: 11-APR-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/323,460  
 ; FILING DATE: 14-OCT-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/11690  
 ; FILING DATE: 14-OCT-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/04178  
 ; FILING DATE: 15-APR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/354,516  
 ; FILING DATE: 21-FEB-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kara, Catherine J.  
 ; REGISTRATION NUMBER: P-41,106  
 ; REFERENCE/DOCKET NUMBER: CPT-004CNI  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 227-7400  
 ; TELEFAX: (617) 227-5941  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 626 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-461-145C-6

Query Match 7.1%; Score 559; DB 3; Length 626;  
 Best Local Similarity 29.9%; Pred. No. 1.8e-28;  
 Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;

QY 1016 SASPQQRKFSLOFHRCNCEKNDKSLSPVFTQSRPLPSN-----IHRKP----- 1062  
 DB 110 SSSMKSLRILLLSQDRN---HTSSPHSGVSRQVRIRKPSQAGDINTITYQAPRGRHLS 166  
 QY 1063 -----SRPTPG-----NTSKQGDPSKSNMTLDLSSKCDSDFFCCSSNSSNAVIP 1107  
 DB 167 VSSQNGRSPSPGYPYPERQOHAROG-----SYT-----SINSEGEFTIP 206  
 QY 1108 SDEVTFTPEEKCRLDVNTLNSIEDLLEASMPSSDTVTYFKSEYAVLSP----- 1158  
 DB 207 E-----TSEQCMDPLPSAENSLSGSCSLDRSADSPSFRKSQMSRARSPDNKECS 259  
 QY 1159 -----EKAENDDY-----KDVYNNQCKEKEAEDEEALAI---AMAMASQ 1199  
 DB 260 DRETQLYDKGVKGTYPRRYHVSVHHKDYNDGRRTPPIRRHOGNLFLLVPSRSLSSTNG 319  
 QY 1200 DALPIYPO-----LQVNGEDIITIQDTPETLPGHTRAKOPYREDETEMLKGOQIG 1252  
 DB 320 ENMGVAVOYLDPRGRRLRSADSENALTVOERNPT-----KSP-SAPINMRGKLLGG 371  
 QY 1253 AFSSCYQADVGSTGLMAVKQYTYVNTSSQEEVEVALREIRMSHNLHNPITRMIGA 1312  
 DB 372 AGRVYLYCDVDTGRGLRSADSENALTVOERNPT-----KSP-SAPINMRGKLLGG 430  
 QY 1313 TCEKSN--YNLFTEWMASSVAHLISKYGAFFKESVINTTEQLRLSLYHENOITIRDY 1370  
 DB 431 LRDRAEKILITFMEYVPGSVKQDLKAYGALTESYRKYTRQILEKMSYLHSMYIHRDI 490  
 QY 1371 KGANLIDSTGORLRADGAARLAS---KGTAGEFQGLIGTATAPAPRYLKGQOYG 1427  
 DB 491 KGANILRDSAG-NVYKGDGASKRIOTICMSGTGI-----RSYTGTPYMWSPVISSEGG 545  
 QY 1428 RSCDVWSVCALITEMACAPPMNAEKSHNLALIFRIASATTAAPSISHLSPGLRDVALR 1487  
 DB 546 RADVWSLGCITYVEMLTEKPPM-AEYEA--MAAIFRIATOPTNPOLPSHISEGRDF-LR 601



QY 1488 CLELQPODRPSPRELLKH 1505  
Db 602 RIFVEARORPSAEELTH 619

## RESULT 14

US-09-423-890-12  
; Sequence 12, Application US/09423890  
; Patent No. 6312934  
; GENERAL INFORMATION:  
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION  
; TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES  
; FILE REFERENCE: CPI-085CPC  
; CURRENT APPLICATION NUMBER: US/09/423,890  
; PRIOR FILING DATE: 2000-03-06  
; PRIOR APPLICATION NUMBER: USSN 60/078,153  
; PRIOR FILING DATE: 1998-03-16  
; PRIOR APPLICATION NUMBER: USSN 60/099,165  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 626  
; TYPE: PRF  
; ORGANISM: Mus musculus  
US-09-423-890-12

Query Match 7.1%; Score 559; DB 4; Length 626;  
Best Local Similarity 29.9%; Pred. No. 1.8e-28;

Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;

QY 1016 SASPOTQRKESLQFRNCPENKDKSLPVTQSRPLPSSN-----IHRKP----- 1062  
Db 110 SSSMKSLRILLLSQDRN---HTSSPHSGVSRQYRIKPSQSGDINTYQAPERSRLTS 166  
QY 1063 -----SRPTPG-----NTSKQDPSKNSMTLDINSSKCDSDFGSCSSNSSNAVIP 1107  
Db 167 VSSQNPGRSSPPGVPYPERQOHIARQ-----SYT-----SINSGEPTP 206  
QY 1108 SDEIVFTVEEKCRLDVTNELSSIEDLEAMSPSSDTVTFKSEVANLSP----- 1158  
Db 207 E-----TSQCMLDPLLSAENSLSGSCQSLDRSADSPFRKSQMSARSFPDRKECS 259  
QY 1159 -----EKAENDDY-----KDVNNHOKCKEKEAEDEEALAI---AMAMSAQ 1199  
Db 260 DRETQLYDKGVKGGTYPRRYHVSNNHNDYNGRRTFPRIRHOGNLTFLVSSSLSTNG 319  
QY 1200 DALPIVPO-----LOVENGEDIIIIQODTPETLPHTKAKOPYREDTEMLKGOQIGLG 1252  
Db 320 ENMGVAOVYLDPRGRRLRSADSENALTVOERNVPT-----KSP-SAPINNRGKLLGQ 371  
QY 1253 AFSSCYQAOVDGTGLMAVKNQVTVYRNTSSQOEVEALREIRMSHLNPNITRMIGA 1312  
Db 372 AFGVYLCYDVTGRELASKOVQFDPD-SPTSKESVSALECEIOLKMLQHERIVQYGC 430  
QY 1313 TCESKN--YNLFIEWMAAGSVAHLISKYGAKESEVINVYTBOLLRGSLYLEHNOIIRHDV 1370  
Db 431 LRDRAREKILTFIEMFMPGGSVKDQKAYGALTESYTRKTYQIIEGMSYILSNMIVHDI 490  
QY 1371 KGANILLDSTQRLRIADFGAARLAS---KGTGAGEFQGLGTIAFMADEVLRGOQYG 1427  
Db 491 KGANILDRSAG-NVYLDGFGASKRLQITICMSGTGI---RSVTGTPYMSPEVVISGEGYG 545  
QY 1428 RSCVWWSGCAIIEMACAKPPMNAEKSHNHLALIFKIASATTAIPSHLSPLGRDVALR 1487  
Db 546 KKADVWSIGCTVVEMLTEKPPW-AEYEA--MAAIFKIAOTPTNPOLPSHISEHGRDF-LR 601  
QY 1488 CLELQPODRPSPRELLKH 1505  
Db 602 RIFVEARORPSAEELTH 619

## RESULT 15

US-08-628-829-10  
; Sequence 10, Application US/08628829A  
; Patent No. 6333170  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Gary L.  
; TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To Exter  
; FILE REFERENCE: CPI-004DPC3  
; CURRENT APPLICATION NUMBER: US/08/628,829A  
; CURRENT FILING DATE: 1996-04-05  
; EARLIER APPLICATION NUMBER: 08/440,421  
; EARLIER FILING DATE: 1995-05-15  
; EARLIER APPLICATION NUMBER: 08/323,460  
; EARLIER FILING DATE: 1994-10-14  
; EARLIER APPLICATION NUMBER: 08/049,254  
; EARLIER FILING DATE: 1993-05-15  
; EARLIER APPLICATION NUMBER: 08/410,602  
; EARLIER FILING DATE: 1995-04-24  
; EARLIER APPLICATION NUMBER: 08/472,934  
; EARLIER FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 626  
; TYPE: PRF  
; ORGANISM: Mus musculus  
US-08-628-829-10

Query Match 7.1%; Score 559; DB 4; Length 626;  
Best Local Similarity 29.9%; Pred. No. 1.8e-28;

Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;

QY 1016 SASPOTQRKESLQFRNCPENKDKSLPVTQSRPLPSSN-----IHRKP----- 1062  
Db 110 SSSMKSLRILLLSQDRN---HTSSPHSGVSRQYRIKPSQSGDINTYQAPERSRLTS 166  
QY 1063 -----SRPTPG-----NTSKQDPSKNSMTLDINSSKCDSDFGSCSSNSSNAVIP 1107  
Db 167 VSSQNPGRSSPPGVPYPERQOHIARQ-----SYT-----SINSGEPTP 206  
QY 1108 SDEIVFTVEEKCRLDVTNELSSIEDLEAMSPSSDTVTFKSEVANLSP----- 1158  
Db 207 E-----TSQCMLDPLLSAENSLSGSCQSLDRSADSPFRKSQMSARSFPDRKECS 259  
QY 1159 -----EKAENDDY-----KDVNNHOKCKEKEAEDEEALAI---AMAMSAQ 1199  
Db 260 DRETQLYDKGVKGGTYPRRYHVSNNHNDYNGRRTFPRIRHOGNLTFLVSSSLSTNG 319  
QY 1200 DALPIVPO-----LOVENGEDIIIIQODTPETLPHTKAKOPYREDTEMLKGOQIGLG 1252  
Db 320 ENMGVAOVYLDPRGRRLRSADSENALTVOERNVPT-----KSP-SAPINNRGKLLGQ 371  
QY 1253 AFSSCYQAOVDGTGLMAVKNQVTVYRNTSSQOEVEALREIRMSHLNPNITRMIGA 1312  
Db 372 AFGVYLCYDVTGRELASKOVQFDPD-SPTSKESVSALECEIOLKMLQHERIVQYGC 430  
QY 1313 TCESKN--YNLFIEWMAAGSVAHLISKYGAKESEVINVYTBOLLRGSLYLEHNOIIRHDV 1370  
Db 431 LRDRAREKILTFIEMFMPGGSVKDQKAYGALTESYTRKTYQIIEGMSYILSNMIVHDI 490  
QY 1371 KGANILLDSTQRLRIADFGAARLAS---KGTGAGEFQGLGTIAFMADEVLRGOQYG 1427  
Db 491 KGANILDRSAG-NVYLDGFGASKRLQITICMSGTGI---RSVTGTPYMSPEVVISGEGYG 545  
QY 1428 RSCVWWSGCAIIEMACAKPPMNAEKSHNHLALIFKIASATTAIPSHLSPLGRDVALR 1487  
Db 546 KKADVWSIGCTVVEMLTEKPPW-AEYEA--MAAIFKIAOTPTNPOLPSHISEHGRDF-LR 601  
QY 1488 CLELQPODRPSPRELLKH 1505  
Db 602 RIFVEARORPSAEELTH 619

Search completed: December 20, 2002, 16:23:31  
Job time : 41 secs

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GenCore version 5.1.3  
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# OM protein - protein search, using sw model

Run on: December 20, 2002, 16:20:40 ; Search time 52 Seconds

(without alignments)  
3874.518 Million cell updates/sec

Title: US-09-697-898-2

Perfect score: 7825  
Sequence: 1 MAAAGNRASSSGFPEARAT.....PDRPPRELLHPRFTTW 1512

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
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19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7515	96.0	1495	22	ABG04377
2	7515	96.0	1495	22	AA604377
3	7515	96.0	1495	23	AA604377
4	6912.5	88.3	1493	20	AA126234
5	6912.5	88.3	1493	20	AA126234
6	6867	85.2	1593	23	AA448935
7	6867	85.2	1593	23	AA448935
8	6318.5	80.7	1302	20	AA42104
9	6318.5	80.7	1302	20	AA42104
10	3102.5	39.6	672	15	AA66029

11	3102.5	39.6	672	19	AA56157	A murine mtogen-a
12	3102.5	39.6	672	20	AA43318	Mitogen ERK kinase
13	3102.5	39.6	672	20	AA43318	Mitogen ERK kinase
14	3102.5	39.6	672	21	AA43318	Mitogen ERK kinase
15	3102.5	39.6	672	21	AA43318	Mitogen ERK kinase
16	3098.5	39.6	672	21	AA43318	Mitogen ERK kinase
17	2475.5	31.6	649	22	AA43318	Mitogen ERK kinase
18	2475.5	31.6	649	22	AA43318	Mitogen ERK kinase
19	595.5	7.6	690	14	AA40974	Novel human diago
20	587.5	7.5	642	21	AA470101	STE11 protein phos
21	578	7.4	651	21	AA477941	Tobacco MAP kinase
22	578	7.4	651	21	AA477941	A. thaliana MAP ki
23	576	7.4	661	21	AA470100	A. thaliana MAP ki
24	559	7.1	626	19	AA470098	A. thaliana MAP ki
25	559	7.1	626	19	AA470098	A. thaliana MAP ki
26	559	7.1	626	20	AA433320	Mitogen ERK kinase
27	559	7.1	626	20	AA433320	Mitogen ERK kinase
28	559	7.1	626	20	AA433320	Mitogen ERK kinase
29	559	7.1	626	21	AA433320	Mitogen ERK kinase
30	558.5	7.1	626	23	AA433320	Mitogen ERK kinase
31	557.5	7.1	626	21	AA433320	Mitogen ERK kinase
32	543	6.9	619	19	AA433320	Mitogen ERK kinase
33	543	6.9	619	20	AA433320	Mitogen ERK kinase
34	543	6.9	619	21	AA433320	Mitogen ERK kinase
35	543	6.9	619	21	AA433320	Mitogen ERK kinase
36	536.5	6.9	619	23	AA433320	Mitogen ERK kinase
37	534.5	6.8	626	20	AA433320	Mitogen ERK kinase
38	531	6.8	619	19	AA433320	Mitogen ERK kinase
39	531	6.8	619	20	AA433320	Mitogen ERK kinase
40	531	6.8	619	20	AA433320	Mitogen ERK kinase
41	531	6.8	619	20	AA433320	Mitogen ERK kinase
42	531	6.8	619	20	AA433320	Mitogen ERK kinase
43	531	6.8	619	20	AA433320	Mitogen ERK kinase
44	530	6.8	619	20	AA433320	Mitogen ERK kinase
45	529.5	6.8	423	22	AA433320	Mitogen ERK kinase

## ALIGNMENTS

RESULT 1	ABG04377	standard; Protein: 1495 AA.
ID	ABG04377	
XX	ABG04377	
AC	ABG04377	
XX	13-FEB-2002	(first entry)
XX	Novel human diagnostic protein #4368.	
XX	Human; chromosome mapping; gene therapy; forensic;	
KW	food supplement; medical imaging; diagnostic; genetic disorder.	
XX	Homo sapiens.	
OS	WO200175067-A2.	
PN	11-OCT-2001.	
PD	30-MAR-2001; 2001WO-US08631.	
PF	31-MAR-2000; 2000US-0540217.	
XX	23-AUG-2000; 2000US-0649167.	
PR	(HYSE-) HYSEQ INC.	
PA	Dymanac RT, Liu C, Tang YT;	
XX	WPI; 2001-639362/73.	
XX	N-PSDB; AAS68564.	
DR	New isolated polynucleotide and encoded polypeptides; useful in	
XX	diagnostics, forensics, gene mapping, identification of mutations	
PT		

PT responsible for genetic disorders or other traits and to assess  
XX blood diversity  
PS Claim 20: SEQ ID No 34736; 103bp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 1495 AA;  
Query Match 96.0%; Score 7515; DB 22: Length 1495;  
Best Local Similarity 97.8%; Pred. No. 0;  
Matches 1461; Conservative 3; Mismatches 28; Indels 2; Gaps 2;  
QY 21 SEAGGGGAGLAKASAPAAAGLREAGSGRERADWRRLRKYRVELDQLEPEPLF 80  
DB 2 SEAGGGGAGLAKASAPAAAGLREAGSGRERADWRRLRKYRVELDQLEPEPLF 61  
QY 81 AASPAASSTSPSPADAAAGSGTGPOVAVPPHGAASGGAHLTESVAAAPSGASSPA 140  
DB 62 AASPAASSTSPSPADAAAGSGTGPOVAVPPHGAASGGAHLTESVAAAPSGASSPA 121  
QY 141 AEPGERAPAAPSPAAAPAGREMEKKTGKLGKMDDRPERMIREKATACMPMKHE 200  
DB 122 AEPGERAPAAPSPAAAPAGREMEKKTGKLGKMDDRPERMIREKATACMPMKHE 181  
QY 201 WERRNRGPPVAVKPIPVKGDSEMNHLAESPGEVOASASPASKGRSPSPGNSPSGR 260  
DB 182 WERRNRGPPVAVKPIPVKGDSEMNHLAESPGEVOASASPASKGRSPSPGNSPSGR 241  
QY 261 TVKSSPGVRRKRVSPVPPQSGRITPPRRAPSPDGPSPSPETNRVKKVRAKLYLQ 320  
DB 242 TVKSSPGVRRKRVSPVPPQSGRITPPRRAPSPDGPSPSPETNRVKKVRAKLYLQ 301  
QY 321 QIGPNSFLIGDSDPNKYVFYFIPQNSCARGTFCIHLFVMLRVQLPSPDMLRKTL 380  
DB 302 QIGPNSFLIGDSDPNKYVFYFIPQNSCARGTFCIHLFVMLRVQLPSPDMLRKTL 361  
QY 381 KNFEVESLEFQKYHRSRRSRIRKASRNTIQKFVSRMSNSHTLSSSTSTSSSENSIDE 440  
DB 362 KNFEVESLEFQKYHRSRRSRIRKASRNTIQKFVSRMSNSHTLSSSTSTSSSENSIDE 421  
QY 441 QMCPTCLGMDDESLTYCEDGCRNKLHHHCMSIAEECRNRREPLICLCRSKRSHDF 500  
DB 422 QMCPTCLGMDDESLTYCEDGCRNKLHHHCMSIAEECRNRREPLICLCRSKRSHDF 481  
QY 501 YSHETLSPVDSPTSLRAAQOQTVOOQPLAGSRNOESNFTLHYGOQTPPAYKDLAEP 560  
DB 482 YSHETLSPVDSPTSLRAAQOQTVOOQPLAGSRNOESNFTLHYGOQTPPAYKDLAEP 541  
QY 561 IOVFGEMLVGLFSRNWVRENALESLHSDVSGALLANGESTGNSGSSGSSPGSGATS 620  
DB 542 IOVFGEMLVGLFSRNWVRENALESLHSDVSGALLANGESTGNSGSSGSSPGSGATS 601

QY 621 GSSQTSISGDVVEACCSVLNMCADPVYVYVAALKTLRALMYTPCHSLAEIRIKLQRL 680  
DB 602 GSSQTSISGDVVEACCSVLNMCADPVYVYVAALKTLRALMYTPCHSLAEIRIKLQRL 661  
QY 681 QPVVDITLVKCADANSTQSLSTLLECKGAGLANGREITKAGSTIGIGVDVLC 740  
DB 662 QPVVDITLVKCADANSTQSLSTLLECKGAGLANGREITKAGSTIGIGVDVLC 721  
QY 741 ILGNQTESNMNMOELLRLCLDLRLLEFPAAEFPHIVSTVDVSAEVEIRYKLLSLTF 800  
DB 722 ILGNQTESNMNMOELLRLCLDLRLLEFPAAEFPHIVSTVDVSAEVEIRYKLLSLTF 781  
QY 801 ALQSDINSHMWKLSRIYVLSARVTVPHVFSKLEMLSVS- STHTFRRRRLMAI 859  
DB 782 ALQSDINSHMWKLSRIYVLSARVTVPHVFSKLEMLSVS- STHTFRRRRLMAI 841  
QY 860 ADEVEIAEALQIGVEPTDGOQ-DSFLQASVPNNIETENNSPECTVHLETKGLCAT 918  
DB 842 ADEVEIAEALQIGVEPTDGOQ-DSFLQASVPNNIETENNSPECTVHLETKGLCAT 901  
QY 919 KLSASSEDISERLASISVGPSSSTTTTTEQPKPMVOTKGRPHSQCLNSPILSHSOL 978  
DB 902 KLSASSEDISERLASISVGPSSSTTTTTEQPKPMVOTKGRPHSQCLNSPILSHSOL 961  
QY 979 MEPALSTPSSSTPVPAGTATVSKHRLQGFIPCRIPASAPOTQKFSLQFHRNCPEND 1038  
DB 962 MEPALSTPSSSTPVPAGTATVSKHRLQGFIPCRIPASAPOTQKFSLQFHRNCPEND 1021  
QY 1039 SDKLSPVFQSRPLPSNTHRPKSPRTPGNTSKODPDKNSMTLDLNSSCDSEFGS 1098  
DB 1022 SDKLSPVFQSRPLPSNTHRPKSPRTPGNTSKODPDKNSMTLDLNSSCDSEFGS 1081  
QY 1099 SNSSNAVIPSDETVEFTVPEKCRDLVNTLNSIEDLEASMPSSDTTTFSEVAVLSP 1158  
DB 1082 SNSSNAVIPSDETVEFTVPEKCRDLVNTLNSIEDLEASMPSSDTTTFSEVAVLSP 1141  
QY 1159 EKAENDDTYKDVNNHKKCKEKEAEBEALAIAMASASODALPIVPOLOVNGEDIT 1218  
DB 1142 EKAENDDTYKDVNNHKKCKEKEAEBEALAIAMASASODALPIVPOLOVNGEDIT 1201  
QY 1219 IOODPTPETLPGHTKAKOPYREDEMLKGOQIGAFSSCYQADVGTGLMVKOYTYR 1278  
DB 1202 IOODPTPETLPGHTKAKOPYREDEMLKGOQIGAFSSCYQADVGTGLMVKOYTYR 1261  
QY 1279 NTSSEQEEVEALREIRMSHNLNHNITRMLGATCEKSNYNLFIEMAGGSVAHLISKY 1338  
DB 1262 NTSSEQEEVEALREIRMSHNLNHNITRMLGATCEKSNYNLFIEMAGGSVAHLISKY 1321  
QY 1339 GAFKESVINYTEQDLRGSLYHENOIHRDYKGANLLDSTGQRLRIDFGAAALASK 1398  
DB 1322 GAFKESVINYTEQDLRGSLYHENOIHRDYKGANLLDSTGQRLRIDFGAAALASK 1381  
QY 1399 GTGAGFQGLGTTAFMAPEVLRGOQYGRSCDVMSVGAITIMACAKPMAEKSHNL 1458  
DB 1382 GTGAGFQGLGTTAFMAPEVLRGOQYGRSCDVMSVGAITIMACAKPMAEKSHNL 1441  
QY 1459 ALIFKIASATAPISPSHLSPLRDVALRCLELPDRPSEBLKHVPERTTW 1512  
DB 1442 ALIFKIASATAPISPSHLSPLRDVALRCLELPDRPSEBLKHVPERTTW 1495  
RESULT 2  
AAB60291  
ID AAB60291 standard; Protein; 1495 AA.  
XX AAB60291;  
AC  
XX  
DT 06-Apr-2001 (first entry)  
XX  
XX Human MEK1.  
DE Human MEK1.  
XX  
XX Human MEK1; mitogen-activated protein kinase kinase kinase 1;  
KW MEK kinase 1; MAP/Erk kinase kinase 1; pro-apoptotic;  
1191-1572  
catalytic  
down owl

KW	apoptosis signal regulation; programmed cell death;
KW	serine/threonine kinase; MAP kinase cascade; JNK/SAPK;
KW	Jun N-terminal kinase/stress-activated protein kinase;
KW	Bcl-2 substrate; NF-kappa-B-mediated transcription regulation;
KW	expression inhibition; antiense therapy;
KW	hyperproliferative disorder; cancer; inflammation.
XX	
OS	Homo sapiens.
XX	
PN	US6168950-B1.
XX	
PD	02-JAN-2001.
XX	
PE	23-JUL-1999; 99US-0359756.
XX	
PR	23-JUL-1999; 99US-0359756.
XX	
PA	(ISIS-) ISIS PHARM INC.
PI	Monla BP, Cowsett LM, Gaarde W, Ward DT;
XX	
XX	WPI; 2001-122264/13.
DR	N-PSDB; AAF27079.

PT New antiense compound targeting nucleic acid encoding human  
PT myogen-activated protein kinase kinase 1 (MEK1), useful for treating  
PT diseases or conditions associated with MEK1 expression, or preventing  
PT inflammation or tumor formation -  
XX  
Example 15; Column 42-52; 35pp; English.

This sentence represents human MEK1. MEK1 (also known as mitogen-activated protein kinase kinase kinase 1, MEK kinase 1 and MAP/ERK kinase kinase 1) is a dual-specific serine/threonine kinase which mediates cellular responses to mitogenic stimuli, being involved in JNK/SAPK (Jun N-terminal kinase/stress-activated protein kinase) MAP kinase cascades. MEK1 regulates signaling events associated with apoptosis (programmed cell death) and NF-kappa-B, both of which have been associated with the development of hyperproliferative disorders such as cancer. Specifically, MEK1 lies directly downstream of Bcl-2 in an apoptotic signaling cascade, and plays a critical role in the control of NF-kappa-B-mediated transcription at multiple points in the apoptotic cascade. The invention relates to antisense oligonucleotides targeted to the human MEK1 gene, which inhibit its expression. A series of oligonucleotides (AAF27086-AAF27125) were designed to target different regions of the human MEK1 RNA, and were analysed for their effect on MEK1 mRNA levels by quantitative real-time PCR. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with MEK1 expression, such as inflammation, and cancer and other hyperproliferative disorders.

**SQ Sequence 1495 AA;**

Query Match	96.08;	Score 7515;	DB 22;	Length 1495;
Best Local Similarity	97.88;	Pred. No. 0;		
Matches 1461; Conservative	3;	Mismatches 28;	Indels 2;	Gaps 2;

Qy	21	SPBGGGGGALKASSAPAAAAGLLREAGSSGGERADWRRRLRLRVRSVEJDLDEQPLFL	80
Db	2	SPBGGGGGALKASSARAAAAGLLREAGSSGGERADWRRRLRLRVRSVEJDLDEQPLFL	61
Qy	81	AASPASSTSPSPERPADAGSGTGFQPAVAVPPHPCAAASRGANHTESYAAPDSGASSPA	144
Db	62	AASPASSTSPSPERPADAGSGTGFQPAVAVPPHPCAAASRGANHTESYAAPDSGASSPA	122
Qy	141	AEPGERAPAAEPSPAAAPAGREMNKETTGLGHRKMDRPERMRIREKLATCAIPAMKHE	200
Db	122	AEPGERAPAAEPSPAAAPAGREMNKETTGLGHRKMDRPERMRIREKLATCAIPAMKHE	189
Qy	201	WLERNRNGPPVAVPIPKYGGSEEMNHIAESPGCEVCAASAASPASKGRSPSPGNPSGR	266
Db	182	WLERNRNGPPVAVPIPKYGGSEEMNHIAESPGCEVCAASAASPASKGRSPSPGNPSGR	244

QY	261	TVKSEBPGVRRKRVSPVFOGSRITTPRRAPSPDGSPPYSPEETNRVNVKVARBLYLLO	320
Db	242	TVKSEBPGVRRKRVSPVFOGSRITTPRRAPSPDGSPPYSPEETNRVNVKVARBLYLLO	301
QY	321	QIGPNSPFLIGDSDPNKYRYFIFIGPONSICARGFCFCHLLFWMLRYPQLEPSDPLMKRTL	380
Db	302	QIGPNSPFLIGDSDPNKYRYFIFIGPONSICARGFCFCHLLFWMLRYPQLEPSDPLMKRTL	361
QY	381	KNFVESEFLQKYYHRSRRSRIRKAPSRRNTIOKFVSRMSNSHTLSSSSTSSSENSIKDEE	440
Db	362	KNFVESEFLQKYYHRSRRSRIRKAPSRRNTIOKFVSRMSNSHTLSSSSTSSSENSIKDEE	421
QY	441	QMPICILGLMDEESLTVCEDGCRNKLHHHCMSIMAECRRNKEPLICLRCSKMRSHDF	500
Db	422	QMPICILGLMDEESLTVCEDGCRNKLHHHCMSIMAECRRNKEPLICLRCSKMRSHDF	481
QY	501	YSHESLSPYDPSSSLRAAQOOTOQOPLAGSRNOSNFNLTHYGTQOIPPAYKDLAEPW	560
Db	482	YSHESLSPYDPSSSLRAAQOOTOQOPLAGSRNOSNFNLTHYGTQOIPPAYKDLAEPW	541
QY	561	IOVGMELVGLFRRNNNVEMRLRLSHDVSALLLLANGESNGSGSSGSGSGATS	620
Db	542	IOVGMELVGLFRRNNNVEMRLRLSHDVSALLLLANGESNGSGSSGSGSGATS	601
QY	621	GSSQTSISGDVVEACSVLSMWCADPYKKYVAALTKTLNMLVYPPCHSLAERIKLORL	680
Db	602	GSSQTSISGDVVEACSVLSMWCADPYKKYVAALTKTLNMLVYPPCHSLAERIKLORL	661
QY	661	QPVYDTILVWCADANSTQSLSLSTLELCKGAGELAVGREITKAGSIGIGVDVYLC	740
Db	662	QPVYDTILVWCADANSTQSLSLSTLELCKGAGELAVGREITKAGSIGIGVDVYLC	721
QY	741	ILGNOTESNMNOQLGLRCLIDRLLEFPAPFPHTVSDVSOABEVEYRYKKLLSLTF	800
Db	722	ILGNOTESNMNOQLGLRCLIDRLLEFPAPFPHTVSDVSOABEVEYRYKKLLSLTF	781
QY	801	ALQSIDNSHSMVGLSRRIYLSASRMYTVPVPHFSKLEMLSVSS-STHTFRMRRLMAI	859
Db	782	ALQSIDNSHSMVGLSRRIYLSASRMYTVPVPHFSKLEMLSVSSVSTHTFRMRRLMAI	841
QY	860	ADEVEIAEAIOLGYEDTLGDOQ-DSEFQASVPNNYLETENSSPECTVHLEKTKGLCAT	918
Db	842	ADEVEIAEAIOLGYEDTLQROHNSFCRHLPEPTTKPKPORTVPLECTVHLEKTKGLCAT	901
QY	919	KLSASSEDISERLASISVGSSSTTTTTTTTBDQPKMYOTKGPHSOCINSLSLHSHOL	978
Db	902	KLSASSEDISERLARIASIVGSSSTTTTTTTTBDQPKMYOTKGPHSOCINSLSLHSHOL	961
QY	979	MEPALSTPSSSTSPVAGTATDVSKHRLQGFICRIIPASPOQRKFSIQFHRNCPENKD	1038
Db	962	MEPALSTPSSSTSPVAGTATDVSKHRLQGFICRIIPASPOQRKFSIQFHRNCPENKD	1021
QY	1039	SDKLSIPVFTOSRPLPSSNIHRPKPSRPTGENTSKODPSKNSMTLJLNNSSKCDSDFCGS	1098
Db	1022	SDKLSIPVFTOSRPLPSSNIHRPKPSRPTGENTSKODPSKNSMTLJLNNSSKCDSDFCGLS	1081
QY	1099	SNSNAVYLPSEYTFVVEEKCRLADVNTLENSIEDLLASMPSSDPTTYTFKSEVAYLSP	1156
Db	1082	SNSNSCCYTSDIEYTFVVEEKCRLADVNTLENSIEDLLASMPSSDPTTYTFKSEVAYLSP	1141
QY	1159	EKAENDPTYKQDVVHNOKCKEKEAEDEEALATAMASASODALPVPOLQVENEDEDII	1218
Db	1142	EKAENDPTYKQDVVHNOKCKEKEAEDEEALATAMASASOVALPVPOLQVENEDEDII	1201
QY	1219	IOQDTPETLPENTKAKOPRYEDTEWMLKGQOIGLGAFSSCYQAODVGTGLMAVKOYTVR	1278
Db	1202	IOQDTPETLPENTKAKOPRYEDTEWMLKGQOIGLGAFSSCYQAODVGTGLMAVKOYTVR	1261
QY	1279	NTSSEOEYVVALKEELIRMSHSHNHPITIMYGATCEKSNYMLFETMAGGSVAHLLSKY	1338
Db	1262	NTSSEOEYVVALKEELIRMSHSHNHPITIMYGATCEKSNYMLFETMAGGSVAHLLSKY	1321
QY	1339	GAPESEVAVINTEEDLEGLSYLEHNOIIRHDVYGAMILLDSTGQORLIADFEAARLASK	1398

DB 1322 GAFKESVINYITQRLRGISYLHENDIIRHDVAGANLIDSTQRLKIDFGAAARLASK 1381  
 QY 1399 GTGAGFQGGQLGCTIAFMAPVLRGOOYGRSCDWSVGCIIIMACAKPPWNAEKHSNHL 1458  
 DB 1382 GTGAGBFQGGQLGCTIAFMAPVLRGOOYGRSCDWSVGCIIIMACAKPPWNAEKHSNHL 1441  
 QY 1459 ALIFKIASATTAISTISHLSPLGRDVALKCLQPODRPPSRRLKHVFRRTTW 1512  
 DB 1442 ALIFKIASATTAISTISHLSPLGRDVALKCLQPODRPPSRRLKHVFRRTTW 1495

## RESULT 3

AAG80184 standard. Protein; 1495 AA.

AC AAG80184;  
 DT 21-JAN-2002 (first entry)

DE Human MEK kinase MEK1 protein fragment.

KW Oncogene; c-raf-1; human; MEK1; MEK kinase; raf-binding; cytosolic;  
 KW mitogen activated and extracellular stimuli regulated kinase;  
 KW gene therapy; NF-KB suppression; tumour cell proliferation;  
 KW NF-KB-mediated signal cascade.

OS Homo sapiens.

PN WO200179501-A2.

PD 25-OCT-2001.

PF 17-APR-2001; 2001WO-DE01518.

PR 14-APR-2000; 2000DE-1020138.

PA (RAPP/) RAPP U R.

PA (WIRT/) WIRTH T.

PI RAPP UR, WIRTH T;

DR WPI: 2002-017617/02.

DR N-PSDB: AAI68659.

PT New nucleic acid encoding partial raf sequence, useful for identifying  
 PT compounds that block binding of raf to its activating kinase as  
 PT potential anticancer agents

PS Disclosure: Fig 11b-d; 66pp; German.

XX This invention describes a novel nucleic acid (I) that: (i) encodes at  
 CC least one raf partial sequence containing a MEK1 (mitogen activated and  
 CC extracellular stimuli regulated (MEK) kinase) binding site; (ii) encodes  
 CC at least one partial sequence of MEK1 containing a raf binding site;  
 CC (iii) is a silent mutation of (i) or (ii); or (iv) hybridizes to  
 CC (i)-(iii). The products of the invention have cytosolic activity and can  
 CC be used for gene therapy. The products also suppress NF-KB activation  
 CC resulting in inhibition of tumour cell proliferation or transformation.  
 CC (I), or proteins/peptides encoded by them, are useful for identifying  
 CC compounds that block binding of raf to MEK1. These compounds, optionally  
 CC where expressed from gene therapy vectors, are useful in human or  
 CC veterinary medicine for treatment of tumors. Antisense sequences, or  
 CC ribozymes, that bind to (I) are used to inhibit MEK1 activation. Also  
 CC nucleic acid (I') encoding at least a part of raf (or its silent  
 CC mutations or hybridizing sequences) is used to examine interaction of  
 CC encoded proteins with activation of the NF-KB-mediated signal cascade and  
 CC to screen for inhibitors of cell transformation by raf-mediated  
 CC activation of NF-KB. This sequence represents the human MEK1 protein  
 CC described in the method of the invention.

XX Sequence 1495 AA;

Query Match 96.0%; Score 7515; DB 23; Length 1495;  
 Best Local Similarity 97.8%; Pred. No. 0;  
 Matches 1461; Conservative 3; Mismatches 28; Indels 2; Gaps 2;

QY 21 SPBAGGGGALAKASAPAAAGLLREAGSGRRADRRRLKRVSVLELDQLEPDLFL 80  
 DB 2 SPBAGGGGALAKASAPAAAGLLREAGSGRRADRRRLKRVSVLELDQLEPDLFL 61  
 QY 81 AASPPASSTSPSPEDADAAGSGTGFPVAVPPPHGAASRGALHTESVAAPDSGASSPAA 140  
 DB 62 AASPPASSTSPSPEDADAAGSGTGFPVAVPPPHGAASRGALHTESVAAPDSGASSPAA 121  
 QY 141 AEPGEKRAPAEPSPAAAPRGEMENKETLKGHKHDDREEMIRREKIKATCPMAKHE 200  
 DB 122 AEPGEKRAPAEPSPAAAPRGEMENKETLKGHKHDDREEMIRREKIKATCPMAKHE 181  
 QY 201 WLERRNRGRGVVYVKPIPVKDGSEMMHLAESPGEVOASAPASGRSPSGNSPSGR 260  
 DB 182 WLERRNRGRGVVYVKPIPVKDGSEMMHLAESPGEVOASAPASGRSPSGNSPSGR 241  
 QY 261 TVKSESPGVARRKRVSPVFGSGRTTPRRAPSPDGFSPYSPEETNRNVKVMARLYLQ 320  
 DB 242 TVKSESPGVARRKRVSPVFGSGRTTPRRAPSPDGFSPYSPEETNRNVKVMARLYLQ 301  
 QY 321 QIGPNSFLIGDSDPDNKKYRFTIGPONSARGTFCIHLFVMLRVQLPSDMLRKTL 380  
 DB 302 QIGPNSFLIGDSDPDNKKYRFTIGPONSARGTFCIHLFVMLRVQLPSDMLRKTL 361  
 QY 381 KNEFESELPQYKHSRRSRKAPSRNTIOKFVSRMSNSHTLSSSTSSSESIIDEER 440  
 DB 362 KNEFESELPQYKHSRRSRKAPSRNTIOKFVSRMSNSHTLSSSTSSSESIIDEER 421  
 QY 441 QMCPICLLGLMDESLTVCEDGCRNKLHHKCMSIAMEECRRNEPTICPLCRSKWRSHP 500  
 DB 422 QMCPICLLGLMDESLTVCEDGCRNKLHHKCMSIAMEECRRNEPTICPLCRSKWRSHP 481  
 QY 501 YSHELSSPVDSFSLAAAOQTYQOOPLAGSRNOSNRLHYGQOIPPAYKDLAEP 560  
 DB 482 YSHELSSPVDSFSLAAAOQTYQOOPLAGSRNOSNRLHYGQOIPPAYKDLAEP 541  
 QY 561 IOVFGMELVGCLEFSRMNNVREMLRRLSHDVSQALLANGESTGNSGSGSSPSGATS 620  
 DB 542 IOVFGMELVGCLEFSRMNNVREMLRRLSHDVSQALLANGESTGNSGSGSSPSGATS 601  
 QY 621 GSSQTSISGDVYBACCSVLSMWCADPVYKYVAALKTLRAMLVYTPCHSLAERIKLQRL 680  
 DB 602 GSSQTSISGDVYBACCSVLSMWCADPVYKYVAALKTLRAMLVYTPCHSLAERIKLQRL 661  
 QY 681 QPVVDITLVKCADANRTSGLSTILLELCQAGELAVGREILKAGSIGIGVDVYVLC 740  
 DB 662 QPVVDITLVKCADANRTSGLSTILLELCQAGELAVGREILKAGSIGIGVDVYVLC 721  
 QY 741 ILGNQESNMWOLRLCLIDLLLEFPFAEFPHIVSTVDVSOAEVEIRYKLLSLTF 800  
 DB 722 ILGNQESNMWOLRLCLIDLLLEFPFAEFPHIVSTVDVSOAEVEIRYKLLSLTF 781  
 QY 801 ALQSDINSHMWGLSRRIYLSARAVTVPHVSKLEMLSVS-STHETRRRRIMAI 859  
 DB 782 ALQSDINSHMWGLSRRIYLSARAVTVPHVSKLEMLSVS-STHETRRRRIMAI 841  
 QY 860 ADVEYAEIAIQLGVEPTLDGQD-DSFLQASVPNNYLETENNSPECTVHLKTKGLCAT 918  
 DB 842 ADVEYAEIAIQLGVEPTLDGQD-DSFLQASVPNNYLETENNSPECTVHLKTKGLCAT 901  
 QY 919 KLSASSEDISERLARSIVGSSSTTTTTEBPKMVOYTKGPHOCNSSLSHSOL 978  
 DB 902 KLSASSEDISERLARSIVGSSSTTTTTEBPKMVOYTKGPHOCNSSLSHSOL 961  
 QY 979 MPFALSTPSSSTPVPAGTATDYSKHLRLOGFTICRIPASPCQRFSLQFHNCENMD 1038  
 DB 962 MPFALSTPSSSTPVPAGTATDYSKHLRLOGFTICRIPASPCQRFSLQFHNCENMD 1021  
 QY 1039 SDKLSFVFTQSRPLPSSNIRPKPSRPPTGNTSKGQDPSKNSMTLDLNNSSKCDSDSFGCS 1098

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Db 1022 SDKLSPTFTSRLPSSNINRPKSRPTPGNTSKQGPSSKSMPLDLNSSKCDSDSGLS 1081
Qy 1099 SNSNAVIPSEDEVFPVEEKCRLDVNTETLNSIEDLLEASMPSSDPTVTVEKSEVAVLSP 1158
Db 1082 SNSNCCYTSDEFTVEFEKCRDLVNTETLNSIEDLLEASMPSSDPTVTVEKSEVAVLSP 1141
Qy 1159 EKAENDTYADVDVNHNOCKEKKMEAEDEBALAMAMASASODALPIYPOLOVENGEDITII 1218
Db 1142 EKAENDTYADVDVNHNOCKEKKMEAEDEBALAMAMASASOVALPIYPOLOVENGEDITII 1201
Qy 1219 IODTPETLGHTRAKOPYEDTEMLKGQOIGLGAFFSCYOAOVDVGTLMAYKQVTVYR 1278
Db 1202 IQDTPETLGHTRAKOPYEDTEMLKGQOIGLGAFFSCYOAOVDVGTLMAYKQVTVYR 1261
Qy 1279 NTSSEDEVEVEALREETIRMSHLNHPNIIIMLGATCEKSNYNLFIEWMAGSVANHLSTKY 1338
Db 1262 NTSSEGEVEVEALREETIRMSHLNHPNIIIRLGTATCEKSNYNLFIEWMAGSVANHLSTKY 1321
Qy 1339 GAKRESVYVITTEBOLLGLSLYHENOIIHRDYGKANLLIDSTGORKIADFGAARLASK 1398
Db 1322 GAKRESVYVITTEBOLLGLSLYHENOIIHRDYGKANLLIDSTGORKIADFGAARLASK 1381
Qy 1399 GTGAGEFGOLLGFIAPMAPEVLRLGQOYGRSCDVMSVGCATTEMACAKPPNNAEKHSNHL 1458
Db 1382 GTGAGEFGOLLGFIAPMAPEVLRLGQOYGRSCDVMSVGCATTEMACAKPPNNAEKHSNHL 1441
Qy 1459 ALIFKIASATTAAPSIPSHLSPLGLRDVALRCLLEQPODRPSSRELKHPVFRTTW 1512
Db 1442 ALIFKIASATTAAPSIPSHLSPLGLRDVALRCLLEQPODRPSSRELKHPVFRTTW 1495

RESULT 4
AA42107
ID AAY42107 standard; Protein; 1493 AA.
XX
AC AAY42107;
XX
DT 09-DEC-1999 (first entry)
XX
DE Murine MEK1 protein sequence.
XX
KW MEK1; MEK2; MEK3; mitogen-activated protein kinase; MAPK; ERK;
KW extracellular regulated kinase; signal transduction; regulation;
KW MAPK/ERK; MKK; MKK; inflammation; cellular proliferation;
KW differentiation; development; cell death.
XX
OS Mus musculus.
XX
PN W09947666-A2.
XX
PD 23-SEP-1999.
XX
PF 15-MAR-1999; 99MO-US05556.
XX
PR 16-MAR-1998; 98US-0078153.
XX
PR 04-SEP-1998; 98US-0099165.
XX
PA (CADU-) CADUS PHARM CORP.
XX
PI Johnson GL.
XX
DR WPI; 1999-571843/48.
XX
DR N-PSDB; AAZ25072.
XX
PT New human MEK1 polynucleotides and polypeptides, used for regulating
PT signal transduction in cells -
XX
PS Example 1; Fig 4; 159pp; English.
XX
CC The present sequence represents murine mitogen-activated protein kinase/
CC extracellular response kinase (MAPK/ERK) kinase kinase (MEK1),
CC specifically designated MEK1. The MEK1 proteins are used to modulate

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CC and regulate signal transduction in cells, as well as for regulation of
CC gene transcription in a cell encoding MEK1, where the cell is involved
CC in inflammation, regulation of cellular proliferation and
CC differentiation, regulation of development, regulation of cell death or
CC regulation of inflammation. They are also used to prepare antibodies.
CC MEK1 polynucleotides can be used to produce the protein recombinantly
CC and as a source of probes and primers.
XX
SQ Sequence 1493 AA;
Query Match 88.3%; Score 6912.5; DB 20; Length 1493;
Best Local Similarity 89.5%; Pred. No. 0;
Matches 1358; Conservative 47; Mismatches 82; Indels 31; Gaps 11;
Qy 1 MAAAAGNRASSSGEPGAAATSPEA--GGCGALAKASSAPAA-AAGLLREAGSGGREPAD 56
Db 1 MAAAAGNRASSSGEPGAAATSPEAAGGGGGGAGLQSGAPAAAGAAAGLLREAGSGGREPAD 60
Qy 57 WRRQLKRVRSVEIDQLPEQPLFLAAASPPCSTSPSPPEADAAAGARFQPAAGPPPPG 115
Db 61 WRRHVRKRVRSVEIDQLPEQPLFLAAASPPCSTSPSPPEADAAAGARFQPAAGPPPPG 120
Qy 116 AASRGAAHLTRESVAAPDSGASSPAAAEPEKRAPAAPSPPAAPAGREMEKKTLLKGLK 175
Db 121 AASRCGSHSALTAARDSGARSPAGAE-----PS-AAASGRMEKKTLLKGLK 170
Qy 176 MDDRPEERMIREKLTATCMAMKHEMLERRNRRCGVVYVPIPVGDGSEMHLAESPGE 235
Db 171 MEDRPEERMIREKLTATCMAMKHEMLERRNRRCGVVYVPIPVGDGSEMHLAESPGE 230
Qy 236 VQASNAASPASGKRSPPSGNSPGRTRYKSESPGVRRKRVSPVPOSGRITPPRRAPSPDG 295
Db 231 GQAGSAAPAPKGRSPSPSGSPSGRSYKVESPVGRKRVSPVPOSGRITPPRRAPSPDG 290
Qy 296 FSPYSPETNRVYKVMARLYLLOQIGPNFLLGGDSPDKRYVFTIGPONCSGARCPFC 355
Db 291 FSPYSPETNRVYKVMARLYLLOQIGPNFLLGGDSPDKRYVFTIGPONCSGARCPFC 350
Qy 356 IHLFVMLRVFQLEPSDPMRLMKTLKNEVESLFPKYHRSRSSRIKASRYNTQKFSRM 415
Db 351 IHLFVMLRVFQLEPSDPMRLMKTLKNEVESLFPKYHRSRSSRIKASRYNTQKFSRM 410
Qy 416 SNSITLSSSTSTSSSENSIDEEQMCPTCLGLMDEESLTVCEDGRNKLHHKMSIW 475
Db 411 SNSITLSSSTSTSSSENSIDEEQMCPTCLGLMDEESLTVCEDGRNKLHHKMSIW 470
Qy 476 AEECRNRNEPLICPLCRSKWRSHPDYSHLSPPVSPSLAAAOQTVQOQPIAGS-RRN 534
Db 471 AEECRNRNEPLICPLCRSKWRSHPDYSHLSPPVSPSLAAAOQTVQOQPIAGS-RRN 530
Qy 535 QESNENLTHYGTQOIPPAYKDLAEPWIOVFGMELVGCLEFSRMNVRREMARLRLSHDVGA 594
Db 531 QESSFNLFHGTQOIPSAVKDLAEPWIOVFGMELVGCLEFSRMNVRREMARLRLSHDVGA 590
Qy 595 LLLANGESTGNSGGSGSGSPSGGATSGSSQTSISGDVVEACCSVLSMYCADPVYKYVAA 654
Db 591 LLLANGESTGNSGGSGSGSLGASGASGSSOPSISGDVVEACCSVLSMYCADPVYKYVAA 650
Qy 655 LKTLRAMLVYTPCHSLARIKRLQRLRPVVDITLVKCADANSRYSQSLISTYLELCKCKQA 714
Db 651 LKTLRAMLVYTPCHSLARIKRLQRLRPVVDITLVKCADANSRYSQSLISTYLELCKCKQA 710
Qy 715 GELAVGREILKAGSIGIGGVYVNLCLIGNOTESNNMOELGLRLCLIDRLLEFFAEFP 774
Db 711 GELAVGREILKAGSIGIGGVYVNLCLIGNOTESNNMOELGLRLCLIDRLLEFFAEFP 770
Qy 775 HIVSTDVSOAPEVETRYKKLLSLTFALQSIDNSHSMGKLSRRTYSSARNTVTPHYF 834
Db 771 HIVSTDVSOAPEVETRYKKLLSLTFALQSIDNSHSMGKLSRRTYSSARNTVTPHYF 830
Qy 835 SKLEMLSVSSSTHTTTRRRRLMAIADVEVIAEAIQIGVEPTLDGQOOSFLOASVPNNYL 894
Db 831 SKLVYMLNASSSTHTTTRRRRLMAIADVEVIAEAIQIGVEPTLDGQOOSFLOASVPNNYL 889

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QY	895	ETTESPECTVHLEKTKGKLCATKLNASSEDIISERLASISVGFSSTTTTTEOPKP	954
Db	890	---EKSNSLEHTHEKREKGSLATRLSSASSSDIDRLAGVSGLP-----FTTEPKP	941
QY	955	MVORKGRHSQCINLSPSLSHSOLMPALSTPSSTSTSVAGTAITDYSKRLGCFIPCR	1014
Db	942	AVORGRHSQCINLSPSLSHSOLMPALSTPSSTSTSVAGTAITDYSKRLGCFIPCR	995
QY	1015	PSASPOTQRKRSLOFHRRCPEKNCKDLSLPVFQTSRPLPSNINHPRKSPPTPGNTSKOG	1074
Db	996	PSASPOQRKRSLQFORNCSEHRSDQLSPVFQTSRRPPSNINHPRKSPRYOCSTSKLG	1055
QY	1075	DPSKNSMTLDINSSSKCDSCDSFGCCSNSSMAVIPSEDVTFPTPVCEKRLDVNTELNSSIED	1134
Db	1056	DATKSSMTLDIGSASRCDSCDSFGCGNGSGNAVIPSEDVTFPTPVCEKRLDVNTELNSSIED	1115
QY	1135	LLEASMPSSDTTYVFKSSVAALSPKAKENDDTYKDQVNNHOKCKEKKEAEDEEPALATA	1194
Db	1116	LLEASMPSSDTTYVFKSSVAALSPKAKENDDTYKDQVNNHOKCKEKKEAEDEEPALATA	1175
QY	1195	MSASODALPIPOLQVENGEDIIILIQDDTPETTLPGHTKAKOPYREDTEWMLKGOIGLAF	1254
Db	1176	MSAQDALPIPOLQVENGEDIIILIQDDTPETTLPGHTKAKOPYREDTEWMLKGOIGLAF	1235
QY	1255	SSCFOADQGVGTMAVKQVTYVRNTSSSEDEVEVALREETIRMSHLNHPNIIRMIGATC	1314
Db	1236	SSCFOADQGVGTMAVKQVTYVRNTSSSEDEVEVALREETIRMGCHLNHPNIIRMIGATC	1295
QY	1315	EKSNNLTPIEMMAGGSVAHLISKYGARKESVINYTEQOLLRGSLYHENQIITHRDVGAN	1374
Db	1296	EKSNNLTPIEMMAGGSVAHLISKYGARKESVINYTEQOLLRGSLYHENQIITHRDVGAN	1355
QY	1375	LLIDSTGQRLRIADFGAAARLASKGTGAGEFGQLTGTIAPMAEVLRGQOYGRSCDWYS	1434
Db	1356	LLIDSTGQRLRIADFGAAARLASKGTGAGEFGQLTGTIAPMAEVLRGQOYGRSCDWYS	1415
QY	1435	VGAATIEMACAKPPMNNEKSHNLALIFKTASATTAPSISHSIPGRADVALLCTELIQPQ	1494
Db	1416	VGAATIEMACAKPPMNNEKSHNLALIFKTASATTAPSISHSIPGRADVALLCTELIQPQ	1475
QY	1495	DRPSPRELKHVPVRTTW 1512	
Db	1476	DRPSPRELKHVPVRTTW 1493	
 RESULT 5 AAY26234 standard; protein: 1493 AA.			
ID	AAY26234		
XX	AAV26234:		
AC			
XX	03-NOV-1999 (first entry)		
DT			
XX			
DE	Murine MEKK1 protein.		
XX			
KM	Murine Mitogen ERK Kinase Kinase 1 protein; MEKK1; protease;		
KW	extracellular signal regulated kinase; ERK; signal transduction pathway;		
KM	regulation; apoptosis; protein kinase; cleavage; caspase; antibody;		
KW	kinase fragment; mutant MEKK1 protein; NH2-terminal fragment; detection;		
KM	immunoreactive; diagnostic; therapeutic assay; reagent; disorder;		
KW	aberrant modification; mis-regulation; mutation; MEKK1 gene;		
KM	aberrant post-translational modification.		
XX			
OS	Mus sp.		
XX			
FH	Key	Location/Qualifiers	
FT	Cleavage-site	871..874	
FT		/note-"Protease-resistant form of MEKK1 protein	
FT	Active-site	generated by mutation at this site"	
FT		875..1493	
FT		/label="Active-fragment	
FT		/note-"Mediates apoptosis"	
FT			

[illegible]





167 KETLGLHMDRPRERMIREKATCMPAMKHEMLERNRGRPVVVKRIPYKGDSEMN 226  
 121 KETLGLHMDRPRERMIREKATCMPAMKHEMLERNRGRPVVVKRIPYKGDSEMN 180  
 227 HLAASPGEVQASAPASKGRSPGNSPGRTYKSSPPVRRKRVSPVFOGRTRP 286  
 181 HLAASPGEVQASAPASKGRSPGNSPGRTYKSSPPVRRKRVSPVFOGRTRP 240  
 287 PRAPSPGFSFYSPEETNRVKNVRAVLYLLOQIGPNSFLIGDSDPNKYRVETIGPN 346  
 241 PRAPSPGFSFYSPEETNRVKNVRAVLYLLOQIGPNSFLIGDSDPNKYRVETIGPN 300  
 347 CSCAGTCIHLTFMRLRFQLEPSPDPMIMRTKNEFESELYFOKYHSRRSRIRKAPSRN 406  
 301 CSCAGTCIHLTFMRLRFQLEPSPDPMIMRTKNEFESELYFOKYHSRRSRIRKAPSRN 360  
 407 TIOKEVSRMSNSHTLSSSTSTSSSENSIKDEEQMCPICLGMDEESLTYCEGCRNK 466  
 361 TIOKEVSRMSNSHTLSSSTSTSSSENSIKDEEQMCPICLGMDEESLTYCEGCRNK 420  
 467 LHHCMSTIAECCRRNRREPLICPCRSKWRSHDFYSHELSPVDSPLRAAQQOTVQQO 526  
 421 LHHCMSTIAECCRRNRREPLICPCRSKWRSHDFYSHELSPVDSPLRAAQQOTVQQO 480  
 527 PLASRRNOESNFNLTHGTQOIPRAYKDLAPMTIOVFQGMELVGLFSNNMVRMALRR 586  
 481 PLASRRNOESNFNLTHGTQOIPRAYKDLAPMTIOVFQGMELVGLFSNNMVRMALRR 540  
 587 LSHDVSAGALLANGESTNGSGSSPGCATSGSSQTSISGDVVEACCSYLSMVCADP 646  
 541 LSHDVSAGALLANGESTNGSGSSPGCATSGSSQTSISGDVVEACCSYLSMVCADP 600  
 647 VYKVVVALKTIRALVYTPCHSLAEIRIKLQRLQPVDTIIVKCADANSRTSOLISTL 706  
 601 VYKVVVALKTIRALVYTPCHSLAEIRIKLQRLQPVDTIIVKCADANSRTSOLISTL 660  
 707 LELCGQAGELAVGREIKAGSIGIGYDVYVNCILNOTESNNMOELIGRLCLIDRLIL 766  
 661 LELCGQAGELAVGREIKAGSIGIGYDVYVNCILNOTESNNMOELIGRLCLIDRLIL 720  
 767 EEPAEFYHIYSTVDSQAEPEIRYKRLSLTLFALQSIDNSHSMVKGILSRRIYLSARM 826  
 721 EEPAEFYHIYSTVDSQAEPEIRYKRLSLTLFALQSIDNSHSMVKGILSRRIYLSARM 780  
 827 VTTVPHVSKLLEMLSVSS-STHTPTMRRLMADVEYIAEIOLAGYBDTIDGOO-DSF 884  
 781 VTTVPHVSKLLEMLSVSS-STHTPTMRRLMADVEYIAEIOLAGYBDTIDGOO-DSF 840  
 885 LOASVPNNVLETTENSPECTVHLEKTKGICATKLSASSEDISRILASISVSPSSSTT 944  
 841 CRHLEPTTIMKPOKTVPLECTVHLEKTKGICATKLSASSEDISRILARISVSPSSSTT 900  
 945 TTTTTEQPKPMVQTKGRPHSOLNSSLSPSHSOLMPALSPSSSTSPVAGTATDVSKH 1004  
 901 TTTTTEQPKPMVQTKGRPHSOLNSSLSPSHSOLMPALSPSSSTSPVAGTATDVSKH 960  
 1005 RLQGTIPCRISASQOTQKRSLOPHRNCPEKBDKLSPVFTQGRPLPSSNTHPKPSR 1064  
 961 RLQGTIPCRISASQOTQKRSLOPHRNCPEKBDKLSPVFTQGRPLPSSNTHPKPSR 1020  
 1065 PTPGNTSKQGPSPKNSMTLIDNNSSKCDSDFGCSSNSNAVLPSEYFTTPEEKCRIDY 1124  
 1021 PTPGNTSKQGPSPKNSMTLIDNNSSKCDSDFGCSSNSNAVLPSEYFTTPEEKCRIDY 1080  
 1125 NTELNSSIEDLLEASMPSSDVTTFKSEVAVLSPEKANDDTYKDVHNNCKEKEMAE 1184  
 1081 NTELNSSIEDLLEASMPSSDVTTFKSEVAVLSPEKANDDTYKDVHNNCKEKEMAE 1140  
 1185 EEBALATAMASASDALPIYPQLOVENGEDIITIQODTPELPGHTYAKOPYREDTEML 1244  
 1141 EEBALATAMASASDALPIYPQLOVENGEDIITIQODTPELPGHTYAKOPYREDTEML 1200  
 1245 KGQDIGLGFSSCYQAOOVGTGLMAVQVYVYRNTSSGEQEVYDALAEETIRMSHLNHP 1304

1201 KGQDIGLGFSSCYQAOOVGTGLMAVQVYVYRNTSSGEQEVYDALAEETIRMSHLNHP 1260  
 1305 NITIRMGATCEKSNYNLFTEMMAGSVAILSKYCAFRESVYINTTEOLLRLSTLHENO 1364  
 1261 NITIRMGATCEKSNYNLFTEMMAGSVAILSKYCAFRESVYINTTEOLLRLSTLHENO 1320  
 1365 IIRHDVKGANLLIDSTGQRLRIADFGAARLASKGTGAGEFQGLLGTIAFWAPE 1419  
 1321 IIRHDVKGANLLIDSTGQRLRIADFGAARLASKGTGAGEFQGLLGTIAFWAPE 1375  
 RESULT 7  
 ID AAM48935 standard; Protein: 1593 AA.  
 AC AAM48935;  
 DT 19-APR-2002 (first entry)  
 DE Murine MEKK1-2.  
 XX Mouse; MEKK: mitogen ERK kinase enzyme; cancer; neuroprotective;  
 KM autoimmune disease; signal transduction; allergy; inflammation;  
 KM neurological disorder; hormone-related disease; apoptosis; infection;  
 KM cytosolic; immunosuppressive; antiinflammatory; antiallergic;  
 KM nontoxic; antiparkinsonian; contraceptive.  
 OS Mus musculus.  
 XX US6333170-B1.  
 PD 25-DEC-2001.  
 XX 05-APR-1996; 96US-0628829.  
 XX 15-APR-1993; 93US-0049254.  
 PR 14-OCT-1994; 94US-0323460.  
 PR 12-MAY-1995; 95US-0440421.  
 PR 06-JUN-1995; 95US-0472934.  
 PA (NAME-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.  
 XX Johnson GL.  
 F1 WPI; 2002-163179/21.  
 DR N-PSDB; AAL41578.  
 PT New isolated nucleic acid encoding mitogen extracellular  
 signal-regulated kinase kinase, useful for gene therapy of e.g. cancer  
 and for recombinant protein production  
 PS Claim 4; Column 121-130; 125pp; English.  
 XX The present invention provides the protein and coding sequences of a  
 number of murine mitogen extracellular signal-regulated kinase (ERK)  
 kinase kinase (MEKK) enzymes. The sequences can be used to treat a wide  
 range of diseases including cancer, autoimmune diseases, inflammation,  
 allergies, degenerative neurological diseases and hormone-related  
 diseases, and for inhibiting spermatogenesis or oocyte maturation for  
 contraception. The present sequence is the murine MEKK1.2 protein  
 sequence.  
 CC Sequence 1593 AA;  
 XX  
 SO  
 Query Match 85.2%; Score 6667; DB 23; Length 1593;  
 Best Local Similarity 86.3%; Pred. No. 0;  
 Matches 1322; Conservative 49; Mismatches 102; Indels 58; Gaps 13;  
 1 MAAAGNRASSSGFGAATSPEA---GGGGALAKASAPAA-AAGLREAGSGGERAD 56  
 102 MAAAGNRASSSGFGAATAAPAGGGGGGALQSGAPAAAGALREFSGAPSAFT 161



CC regulation of inflammation. They are also used to prepare antibodies.  
 CC MEK1 polynucleotides can be used to produce the protein recombinantly  
 CC and as a source of probes and primers.

XX Sequence 1302 AA;

Query Match 80.7%; Score 6318.5; DB 20; Length 1302;  
 Best Local Similarity 93.4%; Pred No. 0;  
 Matches 1330; Conservative 26; Mismatches 46; Indels 15; Gaps 5;

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OY 196 AKKHEWLERRNRGPVYVPIPVKGGSDPMHLAAESPGEVOAASAPASKGRSPGPN 255
    |||AKKHEWLERRNRGPVYVPIPVKGGSDPMHLAAESPGEVOAASAPASKGRSPGPN 255
Db 1 AKKHEWLERRNRGPVYVPIPVKGGSDPMHLAAESPGEVOAASAPASKGRSPGPN 60

OY 256 SPSGRVKSSEPGVRRKRVSPVPOSGRTTPRRRAPSPGSEFSPYSEETNRNRYKMRAR 315
    |||SPSGRVKSSEPGVRRKRVSPVPOSGRTTPRRRAPSPGSEFSPYSEETNRNRYKMRAR 315
Db 61 SPSGRVKSSEPGVRRKRVSPVPOSGRTTPRRRAPSPGSEFSPYSEETNRNRYKMRAR 120

OY 316 LYLLOOIGPNSFLIGDSDPNKYRVFIPGPNCSARGTFCIHLLFVMLVFOLESPDML 375
    |||LYLLOOIGPNSFLIGDSDPNKYRVFIPGPNCSARGTFCIHLLFVMLVFOLESPDML 375
Db 121 LYLLOOIGPNSFLIGDSDPNKYRVFIPGPNCSARGTFCIHLLFVMLVFOLESPDML 180

OY 376 WRKTLKNFEVESLFOKYHSRRSSRIKAPSRNTIOKFVSHMSNHTLSSSTSTSSSENSI 435
    |||WRKTLKNFEVESLFOKYHSRRSSRIKAPSRNTIOKFVSHMSNHTLSSSTSTSSSENSI 435
Db 181 WRKTLKNFEVESLFOKYHSRRSSRIKAPSRNTIOKFVSHMSNHTLSSSTSTSSSENSI 240

OY 436 KKEEEOCMPCICLGMDESLVCEDEGCNKLHHHMCMTAEBECRRNRPLICPLCRSKW 495
    |||KKEEEOCMPCICLGMDESLVCEDEGCNKLHHHMCMTAEBECRRNRPLICPLCRSKW 495
Db 241 KKEEEOCMPCICLGMDESLVCEDEGCNKLHHHMCMTAEBECRRNRPLICPLCRSKW 300

OY 496 RSHDFYSHLSPPVSPSSSLRAAOOTVQOOPLAGSRROESNFNLTHGTQOIPPAYKD 555
    |||RSHDFYSHLSPPVSPSSSLRAAOOTVQOOPLAGSRROESNFNLTHGTQOIPPAYKD 555
Db 301 RSHDFYSHLSPPVSPSSSLRAAOOTVQOOPLAGSRROESNFNLTHGTQOIPPAYKD 360

OY 556 LAEPMIQVFGMELVGCLEFRNMNVREMLRLSHDVSAGALLANGSTNGSGSGSPS 615
    |||LAEPMIQVFGMELVGCLEFRNMNVREMLRLSHDVSAGALLANGSTNGSGSGSPS 615
Db 361 LAEPMIQVFGMELVGCLEFRNMNVREMLRLSHDVSAGALLANGSTNGSGSGSPS 420

OY 616 GAGTGGSSGTSISGDNVVEACCVSLWVCADPYKYVVAALKTLRLAMLVTPCHSLAERIK 675
    |||GAGTGGSSGTSISGDNVVEACCVSLWVCADPYKYVVAALKTLRLAMLVTPCHSLAERIK 675
Db 421 AAGAGSSGSPSISGDNVVEACCVSLWVCADPYKYVVAALKTLRLAMLVTPCHSLAERIK 480

OY 676 LQRLQPVVDITLVKCADANSRTSOLSTLLELCKGGAETLAVGREILKAGSIGIGVD 735
    |||LQRLQPVVDITLVKCADANSRTSOLSTLLELCKGGAETLAVGREILKAGSIGIGVD 735
Db 481 LQRLQPVVDITLVKCADANSRTSOLSTLLELCKGGAETLAVGREILKAGSIGIGVD 540

OY 736 YVLNCLIQNTESNMWQELLGRCLIDRLLEPAEFYPHIVSTDVSAQAPVEIRYKKLL 795
    |||YVLNCLIQNTESNMWQELLGRCLIDRLLEPAEFYPHIVSTDVSAQAPVEIRYKKLL 795
Db 541 YVLNCLIQNTESNMWQELLGRCLIDRLLEPAEFYPHIVSTDVSAQAPVEIRYKKLL 600

OY 796 SLTTRALOSIDNSHSMVCKLSRRITLSSARMYTYVPHVSKLLEMLSVSSSTHFTMRMR 855
    |||SLTTRALOSIDNSHSMVCKLSRRITLSSARMYTYVPHVSKLLEMLSVSSSTHFTMRMR 855
Db 601 SLTTRALOSIDNSHSMVCKLSRRITLSSARMYTYVPHVSKLLEMLSVSSSTHFTMRMR 660

OY 856 LMAIDVEVEIAEIOGVEDTLDGQODSFLQASVPNNYETETNSPECTVLETKGKL 915
    |||LMAIDVEVEIAEIOGVEDTLDGQODSFLQASVPNNYETETNSPECTVLETKGKL 915
Db 661 LMAIDVEVEIAEIOGVEDTLDGQODSFLQASVPNNYETETNSPECTVLETKGKL 716

OY 916 CATKLASSEDISERLAIISVGPSSSTTTTTPQPKPMVOYTKGPHSQCLNSPLSHH 975
    |||CATKLASSEDISERLAIISVGPSSSTTTTTPQPKPMVOYTKGPHSQCLNSPLSHH 975
Db 717 SATRLASSEDISRLAGVSGVLPS--TTTEQPKAVOTGKGRPHSQCLNSPLS-H 770

OY 976 SOLMPALSTPSSSTPSPVAGTATVSKHRLQGFIPCRIPASAPOTOKKFSIQFHRNCE 1035
    |||SOLMPALSTPSSSTPSPVAGTATVSKHRLQGFIPCRIPASAPOTOKKFSIQFHRNCE 1035
Db 771 AQLMPAPASAPASAPV---DISKHPQAFVPCPKIPASAPOTOKKFSIQFHRNCE 825

OY 1036 NKDSKLSVFTQSRPLPSNTHRPKPSRPTGNTSKOGDSPSKNMTLIDLNSSCQDSE 1095
    |||NKDSKLSVFTQSRPLPSNTHRPKPSRPTGNTSKOGDSPSKNMTLIDLNSSCQDSE 1095
Db 826 HKDSQQLSVFTQSRPPSSNTHRPKPSRPGSTSKLGADAKSSMTLIDLGASACQDSE 885

OY 1096 GCSNSNNAVIPSDETFVPEVEKRLDYNTELNSIEDLILASMPSSDTYTFKSEVAV 1155
    |||GCSNSNNAVIPSDETFVPEVEKRLDYNTELNSIEDLILASMPSSDTYTFKSEVAV 1155
Db 886 GGGGNSGNAVIPSDETFVPEVEKRLDYNTELNSIEDLILASMPSSDTYTFKSEVAV 945

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OY 1156 LSPKENDDTYKDDVNNQCKEKEKEAEEBEALAIAMASADALPIVPOLOVENGED 1215
    |||LSPKENDDTYKDDVNNQCKEKEKEAEEBEALAIAMASADALPIVPOLOVENGED 1215
Db 946 LSPKENDDTYKDDVNNQCKEKEKEAEEBEALAIAMASADALPIVPOLOVENGED 1005

OY 1216 IITIOODPETTPEGHTKAKOPYREDTEWLKGOOIGAFSGCVQADVTGTLMAVKYT 1275
    |||IITIOODPETTPEGHTKAKOPYREDTEWLKGOOIGAFSGCVQADVTGTLMAVKYT 1275
Db 1006 IITIOODPETTPEGHTKAKOPYREDTEWLKGOOIGAFSGCVQADVTGTLMAVKYT 1065

OY 1276 YVRNNTSSQEEVEVALREIRIMKSHLNHPNIIIMLGATCEKSNYNLFIMMAGSYAHL 1335
    |||YVRNNTSSQEEVEVALREIRIMKSHLNHPNIIIMLGATCEKSNYNLFIMMAGSYAHL 1335
Db 1066 YVRNNTSSQEEVEVALREIRIMKSHLNHPNIIIMLGATCEKSNYNLFIMMAGSYAHL 1125

OY 1336 SKYGAFKESVYINTYEQLLRGISTYHENQIIRDYKGANLLIDSTGQRLIDFGAARL 1395
    |||SKYGAFKESVYINTYEQLLRGISTYHENQIIRDYKGANLLIDSTGQRLIDFGAARL 1395
Db 1126 SKYGAFKESVYINTYEQLLRGISTYHENQIIRDYKGANLLIDSTGQRLIDFGAARL 1185

OY 1396 ASKGTGAGEFQOLGTTAFMAPEYLRGQOYRSCDWSVGCALITEMACAPPMNAEKHS 1455
    |||ASKGTGAGEFQOLGTTAFMAPEYLRGQOYRSCDWSVGCALITEMACAPPMNAEKHS 1455
Db 1186 ASKGTGAGEFQOLGTTAFMAPEYLRGQOYRSCDWSVGCALITEMACAPPMNAEKHS 1245

OY 1456 NHLALIFKIASATVAPSIPIPSHLSPLGLRDVALRCLQLOPDRPPSRELLKHPVFRITW 1512
    |||NHLALIFKIASATVAPSIPIPSHLSPLGLRDVALRCLQLOPDRPPSRELLKHPVFRITW 1512
Db 1246 NHLALIFKIASATVAPSIPIPSHLSPLGLRDVALRCLQLOPDRPPSRELLKHPVFRITW 1302

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RESULT 9
ID AAY26235 standard; Protein; 1302 AA.
XX
AC AAY26235;
XX
DT 03-NOV-1999 (first entry)
XX
DE Human MEK1 protein.
XX
KW Human Mitogen ERK Kinase 1 protein; MEK1; protease;
KW extracellular signal regulated kinase; ERK; signal transduction pathway;
KW regulation; apoptosis; protein kinase; cleavage; caspase; antibody;
KW kinase fragment; mutant MEK1 protein; NH2-terminal fragment; detection;
KW immunoreactive; diagnostic; therapeutic assay; reagent; disorder;
KW aberrant modification; mis-regulation; mutation; MEK1 gene;
KW aberrant post-translational modification.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Cleavage-site 681..684
FT /note="protease-resistant form of MEK1 protein
FT generated by mutation at this site"
FT Active-site 685..1303
FT /label="Active-fragment
FT /note="Mediates apoptosis"
XX
PN WO9941385-A1.
XX
PD 19-AUG-1999.
XX
PE 12-FEB-1999; 99WO-US02974.
XX
PR 13-FEB-1998; 98US-0023130.
XX
PA (CADU-) CADUS PHARM CORP.
XX
PI Johnson GL;
XX
DR WPL, 1999-508649/42.
DR N-PSDB; AAX80912.
XX
PT A new mammalian serine-threonine protein kinase for treating
PT disorder characterized by aberration of the enzyme gene
XX
PS Claim 13; Page 130-134; 149pp; English.

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XX The present sequence is a human Mitogen ERK kinase 1 (MEK1)  
 CC protein, which functions to integrate proteases and signal transduction  
 CC pathways involved in the regulation of apoptosis. It is a 196 kDa protein  
 CC kinase, which upon cleavage at Asp 681/684 by caspase generates a 91 kDa  
 CC kinase fragment that induces apoptosis and a 113 kDa NH2-terminal  
 CC fragment. Mutant MEK1 proteins that are resistant to cleavage by caspase  
 CC proteases and capable of inhibiting apoptosis can be produced by  
 CC substituting amino acid residues 681-684 with Alanine. MEK1 proteins and  
 CC antibodies immunoreactive with MEK1 proteins are used in diagnostic and  
 CC therapeutic assays and reagents for detecting and treating disorders  
 CC involving aberrant modification, mis-regulation or mutation of MEK1 gene  
 CC and aberrant post-translational modification of MEK1 protein.  
 XX  
 SQ Sequence 1302 AA;  
 Query Match 80.7%; Score 6318.5; DB 20; Length 1302;  
 Best Local Similarity 93.4%; Pred. No. 0;  
 Matches 1230; Conservative 26; Mismatches 46; Indels 15; Gaps 5;  
 QY 196 AMKHEMLERRRRRCPPVVKIPVKGDSSENNHLLAESPEGEVQASAPASGRSPSPGN 255  
 DB 1 AMKHEMLERRRRRCPPVVKIPVKGDSSENNHLLAESPEGEVQASAPASGRSPSPGN 60  
 QY 256 SPSPRTYKSSPGYRRKRVSPVPOSGRIIPRRAPSPDGSPIYSPETNRNRYKVMAR 315  
 DB 61 SPSPRTYKSSPGYRRKRVSPVPOSGRIIPRRAPSPDGSPIYSPETNRNRYKVMAR 120  
 QY 316 LYLLOQIPNSFLIGDSPDKRYVFIFIGPONGSCARGFCFHLFVMLRYQLPSPDML 375  
 DB 121 LYLLOQIPNSFLIGDSPDKRYVFIFIGPONGSCARGFCFHLFVMLRYQLPSPDML 180  
 QY 376 WRKTLNFEVESLEFQKYHSRRSRRIKAPSRNTLOKFVSRMSNHTLSSSTSTSSSENSI 435  
 DB 181 WRKTLNFEVESLEFQKYHSRRSRRIKAPSRNTLOKFVSRMSNHTLSSSTSTSSSENSI 240  
 QY 436 KDEEEOQPCPTCLGLMDDEESTLVCEDGCRNKLHHCHMSYAEERRRRREPIPLCRSKW 495  
 DB 241 KDEEEOQPCPTCLGLMDDEESTLVCEDGCRNKLHHCHMSYAEERRRRREPIPLCRSKW 300  
 QY 496 RSHDFYSHELSPPVDSFSLRAAQOQTVQOOPLAGSRNDSNNTLHYGQOIPPAYKD 555  
 DB 301 RSHDFYSHELSPPVDSFSLRAAQOQTVQOOPLAGSRNDSNNTLHYGQOIPPAYKD 360  
 QY 556 LAEPMIOVFCMELVGLCFSRMNVREMLRLSHDVSGALLLANGESTGNSGGSGSSPS 615  
 DB 361 LAEPMIOVFCMELVGLCFSRMNVREMLRLSHDVSGALLLANGESTGNSGGSGSSPS 420  
 QY 616 GGATSGSSQTSISGDVYVACCSYLSMYCADPVYVYVAALKTLRAMLYTPCHSLAERIK 675  
 DB 421 AGAASGSSQPSISGDVYVACCSYLSMYCADPVYVYVAALKTLRAMLYTPCHSLAERIK 480  
 QY 676 LQRLLOPVVPTIYKCADANSRTSOLSTSTLELCGQAGELAVGRELAKSGTIGIGVD 735  
 DB 481 LQRLLOPVVPTIYKCADANSRTSOLSTSTLELCGQAGELAVGRELAKSGTIGIGVD 540  
 QY 736 YVINCILIGNOTESNMQELLGRCLIDRLLEPAFEYPHIVSTVDSQAEVEIRYKLL 795  
 DB 541 YVINCILIGNOTESNMQELLGRCLIDRLLEPAFEYPHIVSTVDSQAEVEIRYKLL 600  
 QY 796 SLTLFALQSDINSHSMYKSLRRTYLSARAVTVPHVFSKLEMLSVSSHTFTMRRR 855  
 DB 601 SLTLFALQSDINSHSMYKSLRRTYLSARAVTVPHVFSKLEMLSVSSHTFTMRRR 660  
 QY 856 LMAIADAEVEIAEATOLGEVPTLDGQODSFLQASVPNNVLETTESSPECTVHLEKTKGL 915  
 DB 661 LMAIADAEVEIAEATOLGEVPTLDGQODSFLQASVPNNVLETTESSPECTVHLEKTKGL 716  
 QY 916 CARPLASSEDISERLASISVGPSSSTTTTTEQPKPVQOTKGRHSQCLNSPLSHH 975  
 DB 717 SATRLSASSEDISDRLAGVSVGLPSS-----TTTEQPKPVQOTKGRHSQCLNSPLS-H 770  
 QY 976 SOLMFPALSTPSSSTPVPAGTATDVSKHRLQGIPICRIPASPOTORKISLQHRNCPE 1035

DB 771 AQLMFPAPASPCSSAPSV-----DISKHPQAVPCKIPASPOTORKESLQHRNCSE 825  
 QY 1036 NKDSDDKLSPVYTORRPPSSNHRPKSRPPIPGMTYSOGDPSKSMPLDLNSSKCDSD 1095  
 DB 826 HRDSDQLSPVYTORRPPSSNHRPKSRPPIPGMTYSOGDPSKSMPLDLNSSKCDSD 885  
 QY 1096 GCSNSSNAVPIPSDEYFTVPEEKCRDLVNTLSSIEDLEASMPSSDTPVPEKSEVAV 1155  
 DB 886 GCGGNSGNAVPIPSDEYFTVPEEKCRDLVNTLSSIEDLEASMPSSDTPVPEKSEVAV 945  
 QY 1156 LSPKAEKNDTYSKDVVHNNQCKEKEAEFEALAIMANASADALPIYQLOVENGED 1215  
 DB 946 LSPKAEKNDTYSKDVVHNNQCKEKEAEFEALAIMANASADALPIYQLOVENGED 1005  
 QY 1216 IITIQDPTETPLGHTAKOPYREDTEMLGQOIGLAFSSCYOAOVGTTLMAVROYT 1275  
 DB 1006 IITIQDPTETPLGHTAKOPYREDTEMLGQOIGLAFSSCYOAOVGTTLMAVROYT 1065  
 QY 1276 YVRNTSSEOEVEVVALREBEIRMSHLNHPNIRIMAGATCEKSNLFIEMWAGSVANHL 1335  
 DB 1066 YVRNTSSEOEVEVVALREBEIRMSHLNHPNIRIMAGATCEKSNLFIEMWAGSVANHL 1125  
 QY 1336 SKYAFKESVYINTBQLRGLSTLHENQIIRHDYKGANLLIDSTGRLRIADFGAARL 1395  
 DB 1126 SKYAFKESVYINTBQLRGLSTLHENQIIRHDYKGANLLIDSTGRLRIADFGAARL 1185  
 QY 1396 ASKGTGAGEPQOGLGTAFAPEVLLNGOYGRSCDVWVSCATIIEMWAKPPWNAKHS 1455  
 DB 1186 ASKGTGAGEPQOGLGTAFAPEVLLNGOYGRSCDVWVSCATIIEMWAKPPWNAKHS 1245  
 QY 1456 NHLALIFKIASATTAPSIPIHLSGLRDVALRCLLELOPORPSPRELLKHPVFRTTW 1512  
 DB 1246 NHLALIFKIASATTAPSIPIHLSGLRDVALRCLLELOPORPSPRELLKHPVFRTTW 1302  
 RESULT 10  
 AAR66029  
 ID AAR66029 standard; Protein: 672 AA.  
 XX  
 AC AAR66029;  
 XX  
 DT 28-JUN-1995 (first entry)  
 XX  
 DE Mammalian MEK kinase (MEK1).  
 XX  
 KW MEK kinase; MEK1; mitogen-activated protein kinase regulator;  
 KW MAPK; cell atrophy inhibition; Parkinson's; Alzheimer's; cancer;  
 KW autoimmune diseases; allergies; wound healing; oncogenes;  
 KW tumour agents; neurotropic growth factor.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..210  
 FT /note="amino terminus regulatory domain"  
 FT Region 211..215  
 FT /note="regulatory hinge sequence"  
 FT Domain 401..672  
 FT /note="catalytic domain"  
 PN WO9424159-A.  
 PD 27-OCT-1994.  
 XX  
 PF 15-APR-1994; 94WO-US04178.  
 XX  
 PR 15-APR-1993; 93US-0049254.  
 XX  
 PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.  
 XX  
 PI Johnson GL;  
 XX

DR MPI: 1994-357747/44.  
 DR N-PSDB: AAQ79325.  
 XX New MEK kinase protein and related antibodies and nucleic acid  
 PT regulator of mitogen activated protein kinase, useful  
 PT therapeutically to inhibit cell atrophy, to screen for oncogenes  
 PT etc.  
 XX  
 XX Claim 6: Page 8: 84pp: English.  
 XX  
 XX AAQ79325 encodes AAR6029 the mammalian MEK kinase (MEK1), other  
 CC unique mammalian MEK kinases identified by PCR are described in  
 CC AAR6030 (MEK2), AAR6031 (MEK3) and AAR6032 (MEK4). MEK1 is an  
 CC activator, independent of Raf protein, of mitogen-activated protein  
 CC kinases (MAPK). Inactivation of MEK1 can be used in the treatment  
 CC of some cancers, autoimmune diseases and allergies, while  
 CC stimulation can promote wound healing. MEK1 can also be used to  
 CC alleviate cellular atrophy in Parkinson's or Alzheimer's by acting  
 CC as a neurotrophic growth factor, and to screen for oncogenes and  
 CC tumour agents.  
 CC  
 XX  
 XX Sequence 672 AA:

Query Match 39.6%; Score 3102.5; DB 15; Length 672;  
 Best Local Similarity 89.2%; Pred. No. 1.8e-206;

Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

QY 826 MVTTPVHVSFKLEMLSVSSSTHFTMRRLMAIADEVEIAEIQGVEDTDGQDSFL 885  
 DB 1 MVTAVPAVFSKLVMTMNASGSTHFTMRRLMAIADEVEIAEIQGVEDTDGQDS-L 59  
 QY 886 QASVPNNYLETENSSPECTVHLEKTKGLCATKLSASSEDISERLASISVGPSSSTTTT 945  
 DB 60 QAVAPFSCSCL--ENSLHTVHREKTKGLSATRLSASSEDISDRLAGVSGLPSS--- 112  
 QY 946 TTTTEQPKPMVQTKGRPHQCLNSPLSHSOLMPALSTPSSSTPSPVAGTATDYSKRR 1005  
 DB 113 -TTTEQPKPMVQTKGRPHQCLNSPLS-HAQLMPAPAPCSAPSV-----DISKRR 165  
 QY 1006 LOGEIPCRIPSPAPQTKRFSLOFHRNCPENKDSKLSLSPFTQSRPLSPSSNIHRPSPR 1065  
 DB 166 POAFVPCIKIPSPAPQTKRFSLOFHRNCPENKDSKLSLSPFTQSRPSPSSNIHRPSPR 225  
 QY 1066 TTGNSSKODPKSNMTLNLSSKCDSDFGCSNSNNAVIPSDVETFPVEKCKRLDVN 1125  
 DB 226 VEGSTSKLDATKSSMTLDGASRCDDSDFGGSGNNAVIPSDVETFPVEKCKRLDVN 285  
 QY 1126 TELNSSIEDLEBASMPSDDTYTFKSEVAVLSPEKAENDDTYKDVNNHOKCKEKEAE 1185  
 DB 286 TELNSSIEDLEBASMPSDDTYTFKSEVAVLSPEKAENDDTYKDVNNHOKCKEKEAE 345  
 QY 1186 EEPALATAMASASQDALPIVPOLOVENGEDIIIIQODTPELPGHTKAKOPYREDTEWLK 1245  
 DB 346 EEPALATAMASASQDALPIVPOLOVENGEDIIIIQODTPELPGHTKAKOPYREDTEWLK 405  
 QY 1246 GGOIGIGASCSYQADVGTGTLMAVKQVTVYRNSSSEDEVEAEAREIRMMSHLNHN 1305  
 DB 406 GGOIGIGASCSYQADVGTGTLMAVKQVTVYRNSSSEDEVEAEAREIRMMSHLNHN 465  
 QY 1306 IIRMLGATCEKSNYNLFIMMAGGSVAHLSTKYGAFKESVINYTBQLRGLSLYHENOI 1365  
 DB 466 IIRMLGATCEKSNYNLFIMMAGGSVAHLSTKYGAFKESVINYTBQLRGLSLYHENOI 525  
 QY 1366 IIRDVKGANLLIDSTGQRLRIADFGAARLASKGTGAGFQGLGTIAFMAREVLRGQO 1425  
 DB 526 IIRDVKGANLLIDSTGQRLRIADFGAARLASKGTGAGFQGLGTIAFMAREVLRGQO 585  
 QY 1426 YVRSCDVMVSGCAITTEMAKAPPMNAEKSHNHLFEKTLASATYASISHSPLGRDVA 1485  
 DB 586 YVRSCDVMVSGCAITTEMAKAPPMNAEKSHNHLFEKTLASATYASISHSPLGRDVA 645  
 QY 1486 LRCLLEQPDPRPSPRELKHPVFRTTW 1512  
 DB :|||||

DB 646 VRCLLEQPDPRPSPRELKHPVFRTTW 672

RESULT 11

ID AAM56157 standard; protein; 672 AA.

XX AAM56157;

DT 17-JUL-1998 (first entry)

DE A murine mitogen-activated protein kinase kinase (MAPKK).

KW Mitogen-activated protein kinase kinase; MAPKK; mouse;

KW extracellular signal-regulated kinase kinase; MEKK; regulation;

KW signal transduction; raf-independent arm; screening assay; treatment;

KW disorder; cancer; autoimmune disease; inflammation; allergy;

KW neuronal disease; Parkinson's disease; Alzheimer's disease; ds.

OS Mus sp.

PN US5753446-A.

PD 19-MAY-1998.

PF 06-JUN-1995; 95US-0472934.

PR 15-APR-1993; 93US-0049254.

PR 14-OCT-1994; 94US-0323460.

PR 21-FEB-1995; 95US-0354516.

PR 12-MAY-1995; 95US-0440421.

PA (NAE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

PI Johnson GL.

DR MPI: 1998-311395/27.

DR N-PSDB: AAY22676.

XX screening assay for regulators of MEK1 signal transduction - using

PT mammalian MEK1 polypeptide

PS Claim 13; Columns 33-38; 48pp; English.

The present sequence represents a murine mitogen-activated protein kinase kinase (MAPKK) (also known as extracellular signal-regulated kinase kinase (MEKK)). The protein, which is serine/threonine kinase is capable of regulating signal transduction in cells. It regulates the activity of elements of the raf-independent arm of MEK1. A screening assay for compounds that regulate signal transduction by a MEK1 protein comprises contacting a reaction mixture containing a mammalian MEK1 polypeptide and a test compound and determining the effect of the test compound on an indicator of signal transduction by the MEK1 polypeptide in the reaction mixture. Compounds identified by the above assay can be used to prepare therapeutic compositions for treating disorders that are subject to regulation or cure by manipulating a signal transduction pathway in cells involved in the disorders, e.g. cancer, autoimmune diseases, CC inflammations, allergies, and neuronal diseases such as Parkinson's CC disease and Alzheimer's disease.

SO Sequence 672 AA:

Query Match 39.6%; Score 3102.5; DB 19; Length 672;  
 Best Local Similarity 89.2%; Pred. No. 1.8e-206;

Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;

QY 826 MVTTPVHVSFKLEMLSVSSSTHFTMRRLMAIADEVEIAEIQGVEDTDGQDSFL 885  
 DB 1 MVTAVPAVFSKLVMTMNASGSTHFTMRRLMAIADEVEIAEIQGVEDTDGQDS-L 59  
 QY 886 QASVPNNYLETENSSPECTVHLEKTKGLCATKLSASSEDISERLASISVGPSSSTTTT 945  
 DB 60 QAVAPFSCSCL--ENSLHTVHREKTKGLSATRLSASSEDISDRLAGVSGLPSS--- 112

QY	946	TTTTCCPMPVOTGKRPISQCLNSSPSHSHQKLFEPALSTPSSSTPSVPACATADVSKHR	1005
Db	113	-TTTDPQPRPAVOTGKRPISQCLNSSPHS-NQMLPFPAPSAFCSSAPSVP-----DISKHR	165
QY	1006	LOGFICPBPISAPSPOTQRKFSLOFPHRNCPEKDKSLSPVFTQSRPLPSSNIHRKPSRP	1065
Db	166	FOAFVPCBPISAPSPOTQRKFSLOFORNCSEHRSDQSLSPVFTQSRPLPSSNIHRKPSRP	225
QY	1066	TPGNTSKGQDPSKSNMPTLDLNSSSKCDSDSECCSSNSNAVTPSDPYFTTPVEEKCRLDYN	1125
Db	226	VPGSTSKIGDPTKSSMTLDLGSASKCDSDSEFGGNSGNAVTPSDPYFTTPVEDKCRDLVN	285
QY	1126	TELNSISIDLEASPPSSDPTVTFRKSEVAVYSPKAEKNDPTYKDDVHNHOKCKEKFMAEE	1185
Db	286	TELNSISIDLEASPPSSDPTVTFRKSEVAVYSPKAEKNDPTYKDDVHNHOKCKEKFMAEE	345
QY	1186	EEALAIAMAMASASODALPIYPOLQVENGEDI111IQDTPETLPGHTRAKOPYREDTEMLK	1245
Db	346	EEALAIAMAMASASODALPIYPOLQVENGEDI111IQDTPETLPGHTRAKOPYREDTAEMLK	405
QY	1246	GOQIGLGFSSCYAQADYGTGTAAVQVYTVVRNTSSQEEVVALAKREITRMHSHLHNPN	1305
Db	406	GOQIGLGFSSCYAQADYGTGTAAVQVYTVVRNTSSQEEVVALAKREITRMHSHLHNPN	465
QY	1306	IIRMLGATCEKSNYNLFIEMMAGGSVAHLLSKYGAFKESVYINTTEOLLRLSTYHENQI	1365
Db	466	IIRMLGATCEKSNYNLFIEMMAGGSVAHLLSKYGAFKESVYINTTEOLLRLSTYHENQI	525
QY	1366	IHRDVKGANLLIDSTGQRLRIADFGAAARLASKGTGAGEFOGOLLGTATFMAPEVLRGOQ	1425
Db	526	IHRDVKGANLLIDSTGQRLRIADFGAAARLASKGTGAGEFOGOLLGTATFMAPEVLRGOQ	585
QY	1426	YGRSDVWSVGCATIIEMCAKPPMNAEKHSNHLILFIKIASATTAPSTPSHLSPGLDVA	1485
Db	586	YGRSDVWSVGCATIIEMCAKPPMNAEKHSNHLILFIKIASATTAPSTPSHLSPGLDVA	645
QY	1486	LRCLELQAPQDRPPSRKELKHVPFRTTW 1512	
Db	646	VRCLELQAPQDRPPSRKELKHVPFRTTW 672	
RESULT 12			
AY43318			
ID	AA43318	standard; Protein: 672 AA.	
AC	AA43318;		
DT	24-JAN-2000	(first entry)	
DE	Mitogen ERK kinase kinase, MEKK-1, protein sequence.		
KW	Mitogen ERK kinase kinase; MEKK; MEKK-1; neurological disorder; cancer;		
KW	extracellular signal-regulated kinase; inflammation; autoimmune disease;		
KW	allergic reaction; hormone related disease; therapy.		
OS	Mus sp.		
PN	US5981265-A.		
PD	09-NOV-1999.		
PF	05-JUN-1995;	95US-0461146.	
PR	15-APR-1993;	93US-0049254.	
PR	12-MAY-1995;	95US-0440421.	
PR	15-APR-1994;	94WO-US04178.	
PR	14-OCT-1994;	94US-0323460.	
PR	14-OCT-1994;	94WO-US11690.	
PR	28-NOV-1994;	94US-0345516.	
PA	(NAME-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.		

PI	Johnson GL;
XX	
XX	
DR	WPI; 1999-633328/54.
DR	N-PSDB; AAZ31877.
XX	
XX	
PT	Regulating mitogen extracellular signal-regulated kinase kinase protein
PT	activity, useful for the treatment of cancer, neurological diseases and
PT	autoimmune diseases
XX	
PS	Claim 2; Column 49-54; 94pp; English.
XX	
CC	This sequence is the mitogen ERK (extracellular signal-regulated
CC	kinase) kinase kinase-1 (MEK-1). The invention relates to a method of
CC	regulating MEK protein activity in a fungal cell by transforming or
CC	transfecting the cell with a nucleic acid encoding an MEK protein. The
CC	MEK protein is useful for treating cancer, inflammation, neurological
CC	disorders, autoimmune diseases, allergic reactions, and hormone related
CC	diseases.
XX	
SQ	Sequence 672 AA:

Query Match	39.6%;	Score 3102.5;	DB 20;	Length 672;
Best Local Similarity	89.2%;	Pred. No. 1.8e-206;		
Matches 613;	Conservative 21;	Mismatches 38;	Indels 15;	Gaps 5

Oy	826	MVTVPVHVESLLEMLVSSVSTHFTNRBRRLMAIAEVEIAEIAIOLGVEDTLDGGDSFL	885
Dd	1	MVTAVPAVFSKLYMLMASSSTHFTNRKRRRLMAIAEVEIAEYIOLGVEDYVDGQDS-L	59
Oy	886	QASVPNNVLETTENSPECTVHLKTKGKICATKILASSEDIISERLASISVGPSSSTTT	945
Dd	60	QAVAPTSL--ENSSLEHTVHREKTKGKLSATRLASSEDIISDRLAGSVGLPSS---	112
Oy	946	TTTTTEOPKPMVOTGRHSOCLMSSPLSHHSOIMFALSTPSSPMSPVAGATVDSKHR	1005
Dd	113	TTTTTEOPKPAVOTKGRHSOCLMSSPLS-HAQDMFAPSPAPCSSASVY---DISKHR	165
Oy	1006	LOGEIPCRIPSPASPOIORKSTLOQFHRKCEPNKOSDXLSVFOSRPLSPSSNIHRKPSRP	1065
Dd	166	POAVFPCKIPSPASPOIORKFSTLOFORNCSEBHDSDQLSPVFOSRPPSSNIHRKPSRP	225
Oy	1066	TPGNTSKQGPBRSKRSMTLNDLSSKSCDDSPGSCSSNSNAYISDSYETVTPVEKCRLDVN	1123
Dd	226	VPGSTSKIGATKRSMTLNDLSASRCDSPGSGGNSGNAYISDSYETVTPVEKCRLDVN	285
Oy	1126	TELSMSIEDLLEASMPSSDPTTVTFKSEVAALSPKAEKNDYTKDDVNNHOKKEKMEAE	1185
Dd	286	TELSMSIEDLLEASMPSSDPTTVTFKSEVAYALSPKAEKNDYTKDDVNNHOKKEKMEAE	345
Oy	1186	EEALAIAMASASODALPIYPOLQVENGEDI111IQQDPEPLPGHTKAKOPYREDTEWLK	1245
Dd	346	EEALAIAMASASODALPIYPOLQVENGEDI111IQQDPEPLPGHTKAKOPYREDTEWLK	405
Oy	1246	GOQIGLGFASFSCYAOOVGTGTMAAKOVYVYKNTSSBOEVEYVALREIRIMSHLNP	1305
Dd	406	GOQIGLGFASFSCYAOOVGTGTMAAKOYTYVNTSSBOEVEYVALREIRIMAGHLNP	465
Oy	1306	IIRMLGATCEKSNYLPFIEMMAGGSVAHLLSKYGAEKESVYINTYEQLLRGSLYHENQI	1365
Dd	466	IIRMLGATCEKSNYLPFIEMMAGGSVAHLLSKYGAEKESVYINTYEQLLRGSLYHENQI	525
Oy	1366	IHRPVKGNLILIDSTGORTLADPGAAARLASGSGAGEGOOLLGTAFFMAPEVLRQO	1425
Dd	526	IHRPVKGNLILIDSTGORTLADPGAAARLASGSGAGEGOOLLGTAFFMAPEVLRQO	585
Oy	1426	YGRSGDVWSVCAIIEWAKAPPMNAEKHSNHLALFKITASATTAAPSIPSHLSPOLROYA	1485
Dd	586	YGRSGDVWSVCAIIEWAKAPPMNAEKHSNHLALFKITASATTAAPSIPSHLSPOLROYA	645
Oy	1486	LRCLEIOPQDRPPSRRELLKRPVRRTTM 1512	
Dd	646	VRCLEIOPQDRPPSRRELLKRPVRRTTM 672	





PR 21-FEB-1995; 950S-0354516.  
 XX (NAJL-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.  
 PA Johnson GL;  
 XX WPI: 2000-411281/35.  
 DR N-PSDB: AAA49222.  
 XX  
 PT Novel mitogen extracellular signal-regulated kinase kinase (MEKK)  
 PT protein useful for treating cancer, inflammation, autoimmune diseases,  
 PT neurological disorders and hormone related disease in animals  
 XX  
 PS Disclosure; Column 54-56; 92pp; English.  
 XX  
 CC The present sequence is the murine mitogen ERK kinase kinase (MEKK1)  
 CC protein sequence. MEKK1 is involved in a signal transduction pathway  
 CC which can ultimately lead to apoptosis. The proteins regulated by MEKK1  
 CC include the MEK and MAPK proteins and c-Myc. Its coding sequence was  
 CC identified by searching a mouse liver cDNA library for sequences similar  
 CC to the Ste11 and Byr2 genes from yeast (these are MEKK homologues). The  
 CC gene and protein can be used to treat diseases such as cancer,  
 CC autoimmune disease, inflammatory responses, allergic responses and  
 CC neuronal disorders including Parkinson's disease and Alzheimer's disease.  
 XX  
 SQ Sequence 672 AA:  
 Query Match 39.6%; Score 3102.5; DB 21; Length 672;  
 Best Local Similarity 89.2%; Pred. No. 1.8e-206;  
 Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;  
 QY 826 MATTVPVHVSFKLLMLSVSSTHTFTMRRLMAIDVEVEIAEVLQIGVEDTLDGQDSFL 885  
 DB 1 MTTAVPAVVEFSKLTVMASGTHFTMRRLMAIDVEVEIAEVLQIGVEDTLDGQDS-L 59  
 QY 886 QASVPNNYLETNTSSPECTVHLEKTKGICATKLSASSEDISERLASISVGSSTTTT 945  
 DB 60 QAVAPVPSCL--ENSSLEHTVHREKTKGKLSATRLSSASSEDISDRLAGVSGLPSS--- 112  
 QY 946 TTTTEQPKPMVOTKGRPHSQCINSSPLSHNSQMLFPAALSTPSSSTPSVPAGTATDVSKHR 1005  
 DB 113 -TTTEQPKPMVOTKGRPHSQCINSSPLSHNSQMLFPAALSTPSSSTPSVPAGTATDVSKHR 165  
 QY 1006 LQGFICRIPASPTQTKRSLQPHRNCPEKNSDKISLPFTOSRPLPSSNIHPRKPSRP 1065  
 DB 166 PQAFVPCIKIPASPTQTKRSLQPHRNCPEKNSDKISLPFTOSRPLPSSNIHPRKPSRP 225  
 QY 1066 TPQNTSKQGPSPKSNMTLDINSSKCDSDSFGCSNNSNAYIPDEYFTVEKCRIDVN 1125  
 DB 226 VPGSTKLGDAITKSMTLDGASRCDDSGGSGNNAVIPSDEYFTVEKCRIDVN 285  
 QY 1126 TELNSTDIEDLEASMPSSDTTTFKSEVAVLSPKAEKNDTVDYKDVHNNCKCKEKEAE 1185  
 DB 286 TELNSTDIEDLEASMPSSDTTTFKSEVAVLSPKAEKNDTVDYKDVHNNCKCKEKEAE 345  
 QY 1186 EELALATAMMASQDALPIYPOQLQVENGEDIITIOODPTETLPGHTKAKQPIREDEWMLK 1245  
 DB 346 EELALATAMMASQDALPIYPOQLQVENGEDIITIOODPTETLPGHTKAKQPIREDEWMLK 405  
 QY 1246 GQOIGLGAFFSCTQADVDGTLMAVKQVTVYNTSSSEQEVVEALREETRMASHNHPN 1305  
 DB 406 GQOIGLGAFFSCTQADVDGTLMAVKQVTVYNTSSSEQEVVEALREETRMASHNHPN 465  
 QY 1306 IIRMLGATCEKSNYNLEIEMAGGSVAHLISKYGAFFESVIVYTTQDLGLGLYLEHNOI 1365  
 DB 466 IIRMLGATCEKSNYNLEIEMAGGSVAHLISKYGAFFESVIVYTTQDLGLGLYLEHNOI 525  
 QY 1366 IIRHVDVGANLLIDSTGQRRIADFGAAARLASGTGAGEGQGLGTIADMADEVLRGQO 1425  
 DB 526 IIRHVDVGANLLIDSTGQRRIADFGAAARLASGTGAGEGQGLGTIADMADEVLRGQO 585  
 QY 1426 YGRSCDWMSVGCALIEEMACAKPPMNAEKHSNHLALIFKIASATTAPSPHSLPGLRDVA 1485  
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DB 586 YGRSCDWMSVGCALIEEMACAKPPMNAEKHSNHLALIFKIASATTAPSPHSLPGLRDVA 645  
 QY 1486 LRCLLELOPQDRPPSRRLKHPVFTTW 1512  
 DB 646 VRCLLELOPQDRPPSRRLKHPVFTTW 672  
 RESULT 15  
 ID AAA48934  
 AC AAA48934 standard; Protein; 672 AA.  
 AC AAA48934;  
 DT 19-APR-2002 (first entry)  
 DE Murine MEKK1-1.  
 XX Mouse; MEKK1; mitogen ERK kinase kinase; enzyme; cancer; neuroprotective;  
 KW autoimmune disease; signal transduction; allergy; inflammation;  
 KW neurological disorder; hormone-related disease; apoptosis; infection;  
 KW cytosolic; immunosuppressive; antiinflammatory; antiallergic;  
 KW neurotropic; antiparkinsonian; contraceptive.  
 XX  
 OS Mus musculus.  
 XX  
 PN US633170-B1.  
 XX 25-DEC-2001.  
 PD 05-APR-1996; 96US-0628829.  
 PF 15-APR-1993; 93US-0049254.  
 PR 14-OCT-1994; 94US-0323460.  
 PR 12-MAY-1995; 95US-0440421.  
 PR 06-JUN-1995; 95US-0472934.  
 XX (NAJL-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.  
 PA Johnson GL;  
 XX WPI: 2000-163179/21.  
 DR N-PSDB: AAL41577.  
 XX  
 PT New isolated nucleic acid encoding mitogen extracellular  
 PT signal-regulated kinase kinase, useful for gene therapy of e.g. cancer  
 PT and for recombinant protein production  
 XX  
 PS Claim 3; Column 107-110; 125pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of a  
 CC number of murine mitogen extracellular signal-regulated kinase (BRK)  
 CC kinase kinase (MEKK) enzymes. The sequences can be used to treat a wide  
 CC range of diseases including cancer, autoimmune diseases, inflammation,  
 CC allergies, degenerative neurological diseases and hormone-related  
 CC diseases, and for inhibiting spermatogenesis or oocyte maturation for  
 CC contraception. The present sequence is the murine MEKK1.1 protein  
 CC sequence.  
 XX  
 SQ Sequence 672 AA:  
 Query Match 39.6%; Score 3102.5; DB 23; Length 672;  
 Best Local Similarity 89.2%; Pred. No. 1.8e-206;  
 Matches 613; Conservative 21; Mismatches 38; Indels 15; Gaps 5;  
 QY 826 MATTVPVHVSFKLLMLSVSSTHTFTMRRLMAIDVEVEIAEVLQIGVEDTLDGQDSFL 885  
 DB 1 MTTAVPAVVEFSKLTVMASGTHFTMRRLMAIDVEVEIAEVLQIGVEDTLDGQDS-L 59  
 QY 886 QASVPNNYLETNTSSPECTVHLEKTKGICATKLSASSEDISERLASISVGSSTTTT 945  
 DB 60 QAVAPVPSCL--ENSSLEHTVHREKTKGKLSATRLSSASSEDISDRLAGVSGLPSS--- 112  
 QY 946 TTTTEQPKPMVOTKGRPHSQCINSSPLSHNSQMLFPAALSTPSSSTPSVPAGTATDVSKHR 1005  
 |||||||



7-4545

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 16:42:15 ; Search time 173 Seconds  
(without alignments)  
9297.801 Million cell updates/sec

Title: US-09-697-898-1

**Sequence:**

**1** gagaaatggcgcgcgcgc...ttcaaaccaaaaaaaaaa **5245**

Scoring table: IDENTITY\_NUC

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

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6: /cgn2_6/ptodata1/1na/backfiles1.seq: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4564.6	87.0	4693	4	US-09-359-756-1	Sequence 1, Appl
2	3417	65.1	5253	4	US-09-423-890-7	Sequence 7, Appl
3	3387.6	64.6	5539	4	US-08-628-829-3	Sequence 3, Appl
4	3286.4	62.7	3911	4	US-03-423-850-1	Sequence 1, Appl
5	1955.6	37.3	3260	1	US-08-049-254-1	Sequence 1, Appl
6	1955.6	37.3	3260	1	US-08-472-934-1	Sequence 1, Appl
7	1955.6	37.3	3260	2	US-08-333-460A-1	Sequence 1, Appl
8	1955.6	37.3	3260	2	US-08-461-146C-1	Sequence 1, Appl
9	1955.6	37.3	3260	2	US-08-461-145C-1	Sequence 1, Appl
10	1955.6	37.3	3260	4	US-08-628-829-1	Sequence 1, Appl
11	75.8	1.4	2503	1	US-08-472-934-11	Sequence 11, App
12	75.8	1.4	2503	2	US-08-461-146C-11	Sequence 11, App
13	75.8	1.4	2503	3	US-08-461-145C-11	Sequence 11, App
14	75.8	1.4	2503	4	US-08-628-829-7	Sequence 7, Appl
15	74.4	1.4	5236	3	US-03-359-757-1	Sequence 1, Appl
16	73.6	1.4	3089	1	US-08-472-934-5	Sequence 5, Appl
17	73.6	1.4	3089	2	US-08-333-460A-5	Sequence 5, Appl
18	73.6	1.4	3089	3	US-08-461-146C-5	Sequence 5, Appl
19	73.6	1.4	3089	3	US-08-461-145C-5	Sequence 5, Appl
20	73.6	1.4	3089	4	US-08-628-829-9	Sequence 9, Appl
21	73.6	1.4	3332	4	US-03-423-890-11	Sequence 11, App
22	72.8	1.4	4533	4	US-09-171-410-2	Sequence 2, Appl
23	71.6	1.4	2133	4	US-09-488-744A-3	Sequence 3, Appl
24	71	1.4	2465	4	US-09-423-890-9	Sequence 9, Appl
25	71	1.4	2503	1	US-08-472-934-3	Sequence 3, Appl
26	71	1.4	2503	2	US-08-323-460A-3	Sequence 3, Appl
27	71	1.4	2503	2	US-08-461-146C-3	Sequence 3, Appl

28	71	2503	3	US-08-461-145C-3	Sequence 3, Appl 1
29	71	2503	4	US-08-628-829-5	Sequence 5, Appl 1
30	70.4	1.3	4	US-09-423-899-3	Sequence 3, Appl 1
31	64.6	1.935	4	US-09-423-899-5	Sequence 5, Appl 1
32	57.6	1.1	4	US-08-690-477-1	Sequence 1, Appl 1
33	57.6	4.257	4	US-09-250-821A-1	Sequence 1, Appl 1
34	57.6	1.1	4	US-08-843-659-1	Sequence 1, Appl 1
35	57.6	1.1	4	US-09-741-154-3	Sequence 3, Appl 1
36	57.6	1.1	3	US-08-125-468-1	Sequence 1, Appl 1
37	57.6	1.1	30001	US-08-474-933-1	Sequence 1, Appl 1
38	57.6	1.1	2	US-08-369-780-1	Sequence 1, Appl 1
39	57.4	1.1	2248	US-08-475-682-1	Sequence 1, Appl 1
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41	57.4	1.1	2248	US-08-636-036-1	Sequence 1, Appl 1
42	57.4	1.1	2248	US-08-918-509-1	Sequence 1, Appl 1
43	57.4	1.1	2248	US-09-108-263-1	Sequence 1, Appl 1
44	57.4	1.1	4471	US-08-615-942A-1	Sequence 1, Appl 1
45	56.12	1.1	1785	US-08-729-416C-8	Sequence 8, Appl 1

## ALIGNMENTS

```

RESULT 1
US-09-359-756-1
; Sequence 1, Application US/09359756
; Patent No. 6168950
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Donna T. Ward
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF MEK1 EXPRESSION
; FILE REFERENCE: RTS-0077
; CURRENT APPLICATION NUMBER: US/09/359, 756
; CURRENT FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 4693
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4488)
US-09-359-756-1

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Query Match	87.08;	Score 4564.6;	DB 4;	Length 4693;
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Matches 4647;	Conservative 0;	Mismatches 39;	Indels 9;	Gaps 5;
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QY	65	CGAGCCCTGAGGACAGAGCGCGCGGAGGAGGCGCTTCAAGGCGAGGAGGCGCGCGCGGCGTG	124
Db	2	CGAGCCCTGAGGACAGAGCGCGCGGAGGAGGCGCTTCAAGGCGAGGAGGCGCGCGCGGCGTG	61
QY	125	CCGCGGGAACCTGCTGCGGAGGCGGGGACGCGGGGCGCGGAGCGGAGACTGGCGGCGCGC	184
Db	62	CCGCGGGAACCTGCTGCGGAGGCGGGGACGCGGGGCGCGGAGCGGAGACTGGCGGCGCGC	124
QY	185	GGCACCTCGCAAAATGCGGAGTGTGGAGCTGGAGACACTGCTCTGAGAGACCGGCTTTCC	244
Db	122	GGCACCTCGCAAAATGCGGAGTGTGGAGCTGGAGACACTGCTCTGAGAGACCGGCTTTCC	184
QY	245	TTGCGGCTCAACGCGGCGCTCTGACTTCCCGTGCGGAGACCCGAGGACGACGCG	304
Db	182	TTGCGGCTCAACGCGGCGCTCTGACTTCCCGTGCGGAGACCCGAGGACGACGCG	244
QY	305	GGAGTGGGACCGGCGCTTCCAGGCTGTGGGGTGCCGCGCCCGACAGGAAGCCGCGAGCCGGC	364
Db	242	GGAGTGGGACCGGCGCTTCCAGGCTGTGGGGTGCCGCGCCCGACAGGAAGCCGCGAGCCGGC	304
QY	365	GCGGCGCCACCTTACCGAGTGTGGTGCGGCGCGGACGCGGCGCTTCCGAGTCCGCGAG	424
Db	302	GCGGCGCCACCTTACCGAGTGTGGTGCGGCGCGGACGCGGCGCTTCCGAGTCCGCGAG	364

QY	425	CGGCCGACCCGGGAGAAAGCGGCGCCCGCCGCGGAGCCGTCTCTGCAAGCGGCCCG	484
Db	362	CGGCCGACCCCGGGGAGAAAGCGGCGCCCGCCCGCGGAGCCGTCTCTGCAAGCGGCCCG	421
QY	485	CGGCGTGTGAGTGGAGAAATTAAGAAACTCTCAAGGGTTGCAAGAATGGATGATCGTC	544
Db	422	CGGCGTGTGAGTGGAGAAATTAAGAAACTCTCAAGGGTTGCAAGAATGGATGATCGTC	481
QY	545	CAGAGAAACGAATGATCAGGGAGAACTGAAGGCCACCTGTATGCCAGCCTGGAAACAG	604
Db	482	CAGAGAAACGAATGATCAGGGAGAACTGAAGGCCACCTGTATGCCAGCCTGGAAACAG	541
QY	605	AATGGTTGAAAGGAAATATGGCGAGCGCTGTGGTGGTAAAAACCAATCCAGTTAAAG	664
Db	542	AATGGTTGAAAGGAAATATGGCGAGCGCTGTGGTGGTAAAAACCAATCCAGTTAAAG	601
QY	665	GAGATGATCTGMAATGATCACTTACAGCTGAGTCTCCAGAGAGAGTCCAGCAAGTG	724
Db	602	GAGATGATCTGMAATGATCACTTACAGCTGAGTCTCCAGAGAGAGTCCAGCAAGTG	661
QY	725	CGGCTTCAACCACTTCCAAAGGCCGACGCACTCTTCTCTGCAACTCCCAATCAGGTC	784
Db	662	CGGCTTCAACCACTTCCAAAGGCCGACGCACTCTTCTCTGCAACTCCCAATCAGGTC	721
QY	785	GCACAGTAAATACGAATCTCCAGAGTAAGGAAGAAAGAAAGTTGCCCAAGTCCCTTTC	844
Db	722	GCACAGTAAATACGAATCTCCAGAGTAAGGAAGAAAGAAAGTTGCCCAAGTCCCTTTC	781
QY	845	AGAGTGGCAGATCACACACACCCCGGAAGAGCCCTTCCACGAGATGGCTTCTCACATATA	904
Db	782	AGAGTGGCAGATCACACACACCCCGGAAGAGCCCTTCCACGAGATGGCTTCTCACATATA	841
QY	905	GCCCTGAGGAAACAACCCGCGTGTTAACAAAGTGAATGCGGGCCAGACTGTACTTACTGC	964
Db	842	GCCCTGAGGAAACAACCCGCGTGTTAACAAAGTGAATGCGGGCCAGACTGTACTTACTGC	901
QY	965	AGCAATATAGGCGCTTAACCTTCTCTGATTTGGAGAGACACCCCAACATTAATACCGGG	1022
Db	902	AGCAATATAGGCGCTTAACCTTCTCTGATTTGGAGAGACACCCCAACATTAATACCGGG	961
QY	1025	TGTTTATTTGGGCTTCAGAACTGCAGCTGTGCACTGGACATCTTGTATTCATCTCTAT	1088
Db	962	TGTTTATTTGGGCTTCAGAACTGCAGCTGTGCACTGGACATCTTGTATTCATCTCTAT	1022
QY	1085	TTGTGATGCTCCGGGTGTTCACTAACACCTTCAGGCCCAATGTATGAGAAACCTT	1144
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QY	1145	TAAAGAAATTTAGAGTTGAGAGTTGTTCCAGAAATTCACAGTATAGCGTACCTCAAGGA	1209
Db	1082	TAAAGAAATTTAGAGTTGAGAGTTGTTCCAGAAATTCACAGTATAGCGTACCTCAAGGA	1144
QY	1205	TCAAAAGCTCATCTCGTATACACCTCCAGAAAGTTGTTTACGCAATGTCAAAATCTCATAT	1266
Db	1142	TCAAAAGCTCATCTCGTATACACCTCCAGAAAGTTGTTTACGCAATGTCAAAATCTCATAT	1209
QY	1265	CATTGTCATCAATAGTACCTTCTAGCTGTATGTCAGAAACACAGATTAAGGATGAAGAG	1322
Db	1202	CATTGTCATCAATAGTACCTTCTAGCTGTATGTCAGAAACACAGATTAAGGATGAAGAG	1266
QY	1335	AACAGATGTGCTTAATTTGCTTGTGGGCACTGCTGATGTAAGAAAGCTTACAGTGTGG	1388
Db	1262	AACAGATGTGCTTAATTTGCTTGTGGGCACTGCTGATGTAAGAAAGCTTACAGTGTGG	1332
QY	1385	AAGAGCGCTGCAGAGAACAGCTGCACACACATGTGATGTAATTTGGGCAAGAAAGTGTAT	1444
Db	1322	AAGAGCGCTGCAGAGAACAGCTGCACACACATGTGTAATTTGGGCAAGAAAGTGTAT	1388
QY	1445	GAAAGAAATAGAGAACTTTAATATGTCCCTTGTGTATGATTAAGTGGAGATTCATGATT	1509
Db	1382	GAAAGAAATAGAGAACTTTAATATGTCCCTTGTGTATGATTAAGTGGAGATTCATGATT	1444

QY	1505	TCACAGCCACGAATGTCAAGTCCTGTGATTCCTTCCTCCAGAGCTGCACAGC	1564
Db	1442	TCACAGCCACGAATGTCAAGTCCTGTGATTCCTTCCTCCAGAGCTGCACAGC	1501
QY	1565	AGCAACCGTCACACAGAGCTTTGGCTGTGATCAAGAAAGAAATCAAGAGACATTTTAA	1624
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QY	1625	ACCTTACTCATATATGGAACCTCAGCAATCCCTCTCTTACAAAGATTTAGCTGACCAT	1684
Db	1562	ACCTTACTCATATATGGAACCTCAGCAATCCCTCTCTTACAAAGATTTAGCTGACCAT	1621
QY	1685	GGATTCAAGGTCTTTGGAATGGAAGCTGTTGGCTGTATTTTCTAGAAACCTGGAATGTGA	1744
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QY	1745	GAGAGATGGCCCTCAGGCGCTTTCCCATATGTCAAGTGGGGCCCGCTGTGGCAATG	1804
Db	1682	GAGAGATGGCCCTCAGGCGCTTTCCCATATGTCAAGTGGGGCCCGCTGTGGCAATG	1741
QY	1805	GGGAGAGCAGCTGGAATTTCTGGGGGCGAGCAGTGTGAAGACGCCGAGTGGGAGGCACCA	1864
Db	1742	GGGAGAGCAGCTGGAATTTCTGGGGGCGAGCAGTGTGAAGACGCCGAGTGGGAGGCACCA	1801
QY	1885	GTGGGTCTTCCACAGACCAATATCTCAGAGAGATGTGTGAGAGCATGTCCAGCTTCTGT	1924
Db	1802	GTGGGTCTTCCACAGACCAATATCTCAGAGAGATGTGTGAGAGCATGTCCAGCTTCTGT	1861
QY	1925	CAATGTCTGTGCGGACCCGTCTCACAAGATGTAGCTTCTCTCTTAAACATTTGACAG	1984
Db	1862	CAATGTCTGTGCGGACCCGTCTCACAAGATGTAGCTTCTCTCTTAAACATTTGACAG	1921
QY	1985	CCATGTCTGTATATATCTCTTTGGCCACAGTTTATGCGGAAGAAATCAAACTTCAGAGACTTC	2044
Db	1922	CCATGTCTGTATATATCTCTTTGGCCACAGTTTATGCGGAAGAAATCAAACTTCAGAGACTTC	1981
QY	2045	TCACAGCCAGTTTATGACACCATCTCTAGTCAATGTGCAGATGCCAATAGCCGACACATGC	2104
Db	1982	TCACAGCCAGTTTATGACACCATCTCTAGTCAATGTGCAGATGCCAATAGCCGACACATGC	2041
QY	2105	AGCGTCCATATCAACACTGTGTGGAATCTGTGCAAGCGCAACAGAGAGATTTGGCAGTTG	2164
Db	2042	AGCGTCCATATCAACACTGTGTGGAATCTGTGCAAGCGCAACAGAGAGATTTGGCAGTTG	2101
QY	2165	GCAGAGAAATCTAAAAGCTGAGATCCATTGGTATTTGGTGTGATTTATGTCTTAAATTT	2224
Db	2102	GCAGAGAAATCTAAAAGCTGAGATCCATTGGTATTTGGTGTGATTTATGTCTTAAATTT	2161
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QY	2285	TTATATAGATAGACTGTGTGTGGAATTTCTGCTGGAATTTTATCTCATATGTGCACTGTG	2344
Db	2222	TTATATAGATAGACTGTGTGTGGAATTTCTGCTGGAATTTTATCTCATATGTGCACTGTG	2281
QY	2345	ATGTTTCAACAAGCTGACCTCTGTTGGAATCAGATATCAAGATGCTGTCGCCCTTAACT	2404
Db	2282	ATGTTTCAACAAGCTGACCTCTGTTGGAATCAGATATCAAGATGCTGTCGCCCTTAACT	2341
QY	2405	TTGCTTTGCACTCCATTTGAATTTCCCACTCAATGGTTGGCAAACTTTCCAGAGAGATCT	2464
Db	2342	TTGCTTTGCACTCCATTTGAATTTCCCACTCAATGGTTGGCAAACTTTCCAGAGAGATCT	2401
QY	2465	ACTTGAGTCTGCGAAGAAATGGTTACTACAGATACCCATGTGTTTCAAAACCTGTTAGAAA	2524
Db	2402	ACTTGAGTCTGCGAAGAAATGGTTACTACAGATACCCATGTGTTTCAAAACCTGTTAGAAA	2461
QY	2525	TGCTGAGAGTTCACAG--TTCCACATCACTCAACAGATGTGTCGCCGTTGATGGGCTA	2581
Db	2462	TGCTGAGAGTTCACAGTTCACATCACTCAACAGATGTGTCGCCGTTGATGGGCTT	2521
QY	2582	TTGCAAGATGAGGTGGAATTTGCCGAAGCCATCCAGTTGGGCGCTTAAGAACACTTTGATG	2641

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Db 2522 ATGCATAGAGTGGAAATTTGCCGAAGCCATCCAGTTGGGCGTAGAGACATTTTACAAAC 2581
Oy 2642 GTCACAGACAGAC - TTCTTGACGACATCTGTTCCCAACMACTATCTGGAAACACAGA 2699
Db 2582 GACAAACACAAACAGACTTTTGGAGCATCTGTTCCCAACMACTATCTGGAAACACAGA 2641
Oy 2700 GAACAGTTCCTCC - TGAGTGCACAGTCCATTTTAGAGAAACTGGAAAAAGATTATGTGCTA 2758
Db 2642 GAACAGTTCCTCCCTTGAGTGCACAGTCCATTTTAGAGAAACTGGAAAAAGATTATGTGCTA 2701
Oy 2759 CAAAATGAGTGGCAGTTGACAGACATTTCTGAGAGACGTGGCAGCATTTCTGATGAGAC 2818
Db 2702 CAAAATGAGTGGCAGTTGACAGACATTTCTGAGAGACGTGGCAGCATTTCTGATGAGAC 2761
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Db 3902 ATTACAAATCTCTTCAATTTGAATGATGCGAGGGGATCGTGCTCATTTCTGATGAAT 3961
Oy 4019 ATGAGGCTTCAAAAGATCGATGTTTAACTAACACTGAACAGTTACACCGGCGCTTT 4078
Db 3962 ATGAGGCTTCAAAAGATCGATGTTTAACTAACACTGAACAGTTACACCGGCGCTTT 4021
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Oy 4739 ACTAGTCAGAACT 4753
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Db 4679 ACTAGTCAGAACT 4693
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[illegible]

RESULT 3  
US-08-628-829-3  
: Sequence 3, Application US/08628829A  
: Patent No. 6333170

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: GENERAL INFORMATION:
: APPLICANT: Johnson, Gary L.
: TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To Extr
: FILE REFERENCE: CPI-004DVCPI
: CURRENT APPLICATION NUMBER: US/08/628,829A
: EARLIER FILING DATE: 1996-04-05
: EARLIER APPLICATION NUMBER: 08/440,421
: EARLIER FILING DATE: 1995-05-15
: EARLIER APPLICATION NUMBER: 08/323,460
: EARLIER FILING DATE: 1994-10-14
: EARLIER APPLICATION NUMBER: 08/049,254
: EARLIER FILING DATE: 1993-05-15
: EARLIER APPLICATION NUMBER: 08/410,602
: EARLIER FILING DATE: 1995-04-24
: EARLIER APPLICATION NUMBER: 08/472,934
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 5539
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(4779)
: US-08-628-829-3

Query Match      64.6%; Score 3387.6; DB 4; Length 5539;
Best Local Similarity 83.4%; Pred. No. 0;
Matches 4075; Conservative 0; Mismatches 709; Indels 102; Gaps 16;

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QY      61  GCTACGAGCCTGTAGAGCAGCGCGCGCGC-----GGAGAGCCCTCAAGCGAGC 111
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QY      358 GCGGCGAGATCCCGAGCGCGCGCGCGCGCGCGGAGAGAGAGAGACTCTTCACAGGAAAGCGC 417
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QY      112 GCGCGCGCGGCTGCGC--GGACTGCTGCGGAGCGGCGAGCGGCGCGGCGCGAGCGG 168
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QY      169 GCGGACATCGCGCGCGCGCGGACACTGCCCAAAATGCGGAGATGTGAGCTTGACACTGCT 228
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QY      229 GAGAGAGCGCTCTTCCTTGTGCGCGCTCAACCGCGCGGCTTCCTGACT--TCCCGTGGCGG 286
Db      537 GAGAGAGCGCTCTTCCTTGTGCGCGCGCGCGCTTCCTGACT--TCCCGTGGCGG 596

QY      287 AGCCCGGGAGCAGCGGCGGAGTGGACCGGCTTCAGCCCTGTGAGCGTGGCGCGCGCC 346
Db      597 AGCCCGGGAGCGGCTGACAGAGCAGAGTGTGCTTCAGCCCG--CGCGGAGACCGCACCCC 655

QY      347 ACGAGCGCGAGCGCGCGCGCGCGCCACCTTACCGAATCGTGTGGCGCGCGCGGACAGCG 406
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QY      407 GCGGCTGAGATGCGGCGAGCGGCGGAGCGCCCGGAGGAAGCGGCGCGCGCGCGGACGCGT 466
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QY      467 CTCCTGAGCGGCGCGCGCGCGCGCTGATGATGAGAAATTAAGAAACTCTCAAGAGTTGC 526
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Db      806 ACAAGATGAGAGATGCGCCGAGGAGAGAAATGATCCGGAGAACTCAAGCGACCTGTA 865

QY      587 TGGCAGCGCTGAACACAGGAATGCTTGGAAAGGAGAAATAGCGGAGGCGCTGTGGTGTAA 646
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QY 707 GAAGGTCCAGGCAAGTGGCGCTTCACAGCTTCCAAAGGCCAGAGAGTCTTCTCTG 766  
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QY 1664 ACAAAAGATTAGTGAGCCATGATTCAGGTGTTGGAATGGAATGTTGGCTGCTTAT 1723  
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QY 1724 TTTCTAGAAACCTGCAATGTGAGAGATGGCCCTCAGGCGCTCTTTCCTCATGATGTCAAGT 1783  
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QY 1784 GGGCGCTGCTGTGGCAAAATGGGAGAGACACTGGAATTTCTGGGGGAGAGAGTGAAGCA 1843  
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QY 1844 GCCGAGTGGGGAGAGCAGCAGTGGGTCTCCAGACAGTATCTCAGAGATGTGGTGG 1903  
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QY 1904 AGGCACTGCTCAGCGTCTGTCAATGGTGTGCTGACCTGTCTTACAAAGTATGCTTGG 1963  
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QY	2924	CTCATCATCTCCAAATTAAATGTTTCCAGCCCTGTGCAACCCCTTCTCTTCTTACCACATCG	2983
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QY	2984	TACCAAGCTGGCATGCAACAGATGTCTTAAGCATAGACTTCAAGGATTCATTTCCGTCA	3043
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QY	3044	GAATATCCTTGTCATCTCCCAAAACACAGGCAAGTTTCTCTACAAATTCCACAGAAACT	3103
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QY	3104	GTCCTGAAAACAAGACTCAGATAACTTTTCCCACTTTTACTCAGTCAGACAGCCCTTGC	3163
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Db	3401	CCTCGAGTAATATCACAGGCCAAAGCACTCCGACCCCTTCCGGCAGGTACAAACAAAC	3460
QY	3224	AGGAGATCCCTCAAAAATAGCATGACATTTATCTGAAACAGTAACTGTTCCAAATGTATG	3283
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QY	3344	TCACCCCAAGTAGAGGACAAATGCAATGTAGTATCAATTACAGAGTCAACTCCAGTATG	3403
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QY	3404	AGGACCTTTTGAAGCATCTATGCTCTTCAAGTGATCAACAGTAACTTTTAAAGTCAGAG	3463
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Db	3701	TTGCGCTCTCTCTCTCCGAAAAGGCGGAAAATGATACACACTTACAAAGCGAGCTCAATC	3760
QY	3524	ATTAATCAAAAGTGCAAAAGAGAAAGATGGAAGCTGAAAGAAACAAACACTTTAGCAATTGGCA	3583
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QY	3584	TGGCAATGTCAGGCTCTCAGGATGCCCTCCCATAGTTCCTCAGCTGCAGGTTGAAAATG	3643
Db	3821	TGGGATGTCAGGCTCTCAGGATGCCCTCCCATAGTTCCTCAGCTGCAGGTTGAAAATG	3880
QY	3644	GAGAAAGATCATCATTAATTAATCAACAGAGATTAACACAGAGCTCTACAGAGCAATACCAAG	3703
Db	3881	GAGAAAGATTAATTAATTAATTAATCAACAGAGATTAACACAGAGCTCTCTCAGAGCAATACCAAG	3940
QY	3704	CAAAACAACGATATAGAGAGAGCACTGAATGGCTGAAAAGGTCAACAGATAGGCTCTTGAG	3763
Db	3941	CGAAACAGCCCTTAACAGAGAGCGCTGAGTGGCTGAAAAGGCAAGCAATAGGCTCTTGAG	4000
QY	3764	CATTTTCTCTCTGTATTCAGGCTCAAGATGTGGGAATCTGGAACCTTAATAGCTGTGTTAAC	3823
Db	4001	CATTTTCTCTCTGTATTCAGGCTCAAGAGATGTGGGACTGGAACCTTAATAGCTGTGTTAAC	4060
QY	3824	AGGTGACTTAATGTGAGAAACACATCTTCTGAGCAAAACAAATAGTAGAGACACTTAATAG	3883
Db	4061	AGGTGACTTAATGTGAGAAACACATCTCTCGAGAGAGAGAGGTGGTGGAAAGCTTTGAGAG	4120
QY	3884	AAGAGATTAAGATGATGAGCCATCTGAATATCCAAACATCAATAGATGTTGGAGCCA	3943

Db	4121	AAGAGATCCGATATGATGGGTACCTCAACATCCAAACATCATCCGATAGCTGGGGGCA	4180
OY	3944	CGTGTGAGAGAGACGATTTACAATCTCTTCATTGATGATGGCAGGGGAGTCGTTGCCTC	4003
Db	4181	CGTGTGAGAGAGACGATTTACAACCTCTTCATTGATGATGGCAGGGGAGATCTGTGGCTC	4240
OY	4004	ATTGGCTAGTAATTAATTTGAGACCTTCAAAACATCACTAGTATTTAACTCACTGAACGT	4065
Db	4241	ACCTCTTAGTAATTAATTTGAGACCTTTCAAGAGATCACTGCTCATTAATCACTGAGCACT	4300
OY	4064	TACTCGGTGGCTTTGCTATCTCCATGAAAAACCAATTCATTCAAGAGATGTCAAAAGGTG	4123
Db	4301	TACTGCGGTGGCTTTGCTATCTCCAGAGAAACCAATTCATTCAAGAGAGCTCAAAAGGTG	4360
OY	4124	CCAATTGCTAATTAATGACAGACGTGTCAAGACTTAAGAAATTTGCAGATTTTGGAGCTCGAG	4183
Db	4361	CCAACCTGCTAATTAATGACAGACCGGTGTAGAGGTGAGAAATTTGCAGCTTTTGAAGTGTGTG	4420
OY	4184	CCAGGTGTGCGATCAAAAGAAAGTGTGTGACAGAGATTTGAGGACAAATTAATGCGGGACAA	4243
Db	4421	CCAGGTGTGCGATCAAAAGAAACCGGTGTGACAGAGATTTCCAGAGGACAGTTACTGGGGACAA	4488
OY	4244	TTGCATTTATGTGACCTGAGGTACTAAGAGGTCAACAGTATGGAGAGAGCTGTATGTAT	4303
Db	4481	TTGCATTTATGTGACCTGAGGTACTTAAGAGGTGACAGTATGGTATGAGACCTGTATGTAT	4540
OY	4304	GGAGTGTGTGGTGTGCTATTATATGAATAATGGCTGTGCAAAACACCATGAGATGTGAGAA	4365
Db	4541	GGAGTGTGTGGTGTGCGATTTATGAATAATGGCTGTGCAAAACACCATGAGATGTGAGAA	4600
OY	4364	AACACTCCAACTCATCTTGTGCTTTGATATTTAAGATTTCTATGTGCAACTACTGCTTCATCGA	4423
Db	4601	AACACTCCAACTCATCTGCTTATATTTAAGATTTCTATGTGCAACTACTGCACTGCTTC	4660
OY	4424	TCCCTCACTATTTGTCTCCGCGTTTACGAGATGTGGCTCTGTGGTTTATGAACCTTCAC	4483
Db	4661	TCCCTCACTACTCTTCCCCCGGGTCTGCGACGCTGGCGGCTGTGATTAAGAACTTCAC	4720
OY	4484	CTCAGGACAGACCTCCATCAAGAGAGCTACTGAAGCATCCACTCTTTCGTACTACATGCT	4543
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OY	4544	AGCCAAATTTGCGAATCTCAACTACAGTATGAAGAAACAGATGCTCAACAGAGAAAAAACTT	4603
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OY	4779	GCCCTAGGTGAAAGGAAAAACAATGAAGTTTGCATGACTAAATTCGAGNAGCATTAATTT	4838
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OY	4839	ATTTTTTTGGAGCACTTTTTCACGAA	4864
Db	5080	A--TTTTTGGAGCACTTTTTCACCTA	5103

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RESULT 4
US-09-423-890-1
; Sequence 1, Application US/09423890
; Patent No. 6312934
; GENERAL INFORMATION:

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? APPLICANT: CADUS PHARMACEUTICAL CORPORATION  
 ? TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES  
 ? TITLE OF INVENTION: AND USES THEREOF  
 ? FILE REFERENCE: CPT-08SCPC  
 ? CURRENT APPLICATION NUMBER: US/09/423,890  
 ? CURRENT FILING DATE: 2000-03-06  
 ? PRIOR APPLICATION NUMBER: USSN 60/078,153  
 ? PRIOR FILING DATE: 1998-03-16  
 ? PRIOR APPLICATION NUMBER: USSN 60/099,165  
 ? PRIOR FILING DATE: 1998-09-04  
 ? NUMBER OF SEQ ID NOS: 38  
 ? SOFTWARE: PatentIn Ver. 2.0  
 ? SEQ ID NO 1  
 ? LENGTH: 3911  
 ? TYPE: DNA  
 ? ORGANISM: Homo sapiens  
 ? FEATURE:  
 ? NAME/KEY: CDS  
 ? LOCATION: (3)..(3908)  
 ? US-09-423-890-1

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Db 1861 TCTCTCGAGAGATATATCTGAGCTCTGCGAGATGGTGAACCCAGTGGCCGCTGTGTTT 1920  
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Db 1981 GTCGTATGGCTATCCCGGATGAGTAAGAAATGGCCAGGTCTATCCAGCTGGGTGTGAGAG 2040  
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Db 2149 TTAGTGTCTACGAGACTGAGTGGCAGCTGGAGGACATTTCTACAGACTGGCGGCGTCT 2208  
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Db 2254 CGGTCAAAACAAAGGAGAGACCCCAAGTCAAGTGTGTAAGTCTCTTATCTCTTGTGTC--TC 2310  
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Oy 2990 CTGGCAGTGCACAGATGCTCTTAAGCATAGACTTCAAGGATTCATTTCCCTGACAGATAC 3049  
Db 2368 -----CAGATTAATTTCTAAGCACAGACCCAGGACATTTGTCTCTCAAAAATAC 2415  
Oy 3050 CTTCGATCTCTCAACACAGCGCAGTCTTCTCAATTCACAACTGATGACAGT 3109  
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Db 3256 TAAAGATGAGAGCATCTGATCAATCCAAACATTAATGATGTTGGAGCCAGCTGTG 3315  
Oy 3950 AGAAGAGCAATTAATCTCTTCAATTTGAATGATGAGAGGAGGATGGCTCATTTGC 4009  
Db 3316 AGAAGAGCAATTAATCTCTTCAATTTGAATGATGAGAGGAGGATGGCTCATTTGC 3375  
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Oy 4370 CCAATCATCTTCTTGAATTAATTAAGATTGTAGTGAACCTACTGTCATGATCCCT 4429  
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Db 3796 CACATTTGCTCTGCTGTTACAGAGATGGCTCTTGTGTTTAAAGTCAACCTCAGG 3855  
Oy 4490 ACAGACCTTCATCAAGAGAGCTACAGAGCATCCAGTCTTCTGTAATGATGATG 4545  
Db 3856 ACCGGCTTCGCAAGAGAGCTGTAACCAATCCGCTCTTCGTAACAGCTGGTAG 3911

RESULT 5  
US-08-049-254-1

Sequence 1 Application US/08049254  
Patent No. 5405941  
GENERAL INFORMATION:  
APPLICANT: Johnson Ph.D., Gary L.  
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL  
TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SHERIDAN ROSS & MCINTOSH, P.C.  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: CO  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/049,254  
FILING DATE: 19930415  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kovarik Esq., Joseph E.  
REGISTRATION NUMBER: 33,005  
REFERENCE/DOCKET NUMBER: 2879-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
TELEX: 467377  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3260 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MEKK  
STRAIN: murine  
IMMEDIATE SOURCE:  
LIBRARY: mouse liver  
CLONE: MEKK CDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..485  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 486..2501  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 2502..3260



APPLICATION NUMBER: PCT/US94/11690  
 FILING DATE: 14-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/04178  
 FILING DATE: 15-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Giulio A. Decontini, Jr. Esq.  
 REGISTRATION NUMBER: 31,503  
 REFERENCE/DOCKET NUMBER: CPI-004DVCP2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3260 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: MEK  
 STRAIN: murine  
 IMMEDIATE SOURCE:  
 LIBRARY: mouse liver  
 CLONE: MEK CDNA  
 FEATURE:  
 NAME/KEY: 5'UTR  
 LOCATION: 1..485  
 NAME/KEY: CDS  
 LOCATION: 486..2501  
 NAME/KEY: 3'UTR  
 LOCATION: 2502..3260  
 US-08-472-934-1

Query Match 37.3%; Score 1955.6; DB 1; Length 3260;  
 Best Local Similarity 82.7%; Pred. No. 0;  
 Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

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QY 3976 GAATGATGAG 4035  
Db 1935 GAATGATGAG 1994  
QY 4036 TCAGAT 4095  
Db 1995 TCAGAT 2054  
QY 4096 CAAATCATCTAGATGTTGGAGCCAGCTGAGAGAGAGATATATATATATATATATATATATAT 4155  
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QY 4156 CTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4215  
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QY 4276 CAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4335  
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Db 2355 ATTGCTAGGAG 2414  
QY 4456 GTGGCT 4515  
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Db 2595 CCATGATGCTCAACAG 2653

QY 4692 ATTGCAAAATCATGATCTGTACTTAAAGCTCAGTATGCA-AAAGCCCAAACTAGTCCAGAA 4750  
Db 2654 ATTGCAAAATCATGATCTGTACTTAAAGCTCAGTATGCAAGACATCTAAGCTGTCCAGAA 2713  
QY 4751 ACTGTAACCTGAGCTCTTCAAAAGCTGAGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 4810  
Db 2714 ACTGTAACCTGAGCTCTTCAAAAGCTGAGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 2773  
QY 4811 CATGACTAAATATGAG 4864  
Db 2774 CATGACTAAATATGAG 2825

RESULT 7  
US-08-323-460A-1  
Sequence 1, Application US/08323460A  
Patent No. 5854043  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, GARY L.  
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SHERIDAN ROSS & MCINTOSH  
STREET: 1700 LINCOLN STREET, SUITE 3500  
CITY: DENVER  
STATE: CO  
COUNTRY: USA  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/323,460A  
FILING DATE: 14-OCT-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/049,254  
FILING DATE: 14-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOVARIK, JOSEPH E.  
REGISTRATION NUMBER: 33,005  
REFERENCE/DOCKET NUMBER: 2879-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/863-9700  
TELEFAX: 303/863-0223  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3260 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MEK  
STRAIN: murine  
IMMEDIATE SOURCE:  
LIBRARY: mouse liver  
CLONE: MEK CDNA  
FEATURE:  
NAME/KEY: 5'UTR  
NAME/KEY: 1..485  
NAME/KEY: CDS  
LOCATION: 486..2501  
NAME/KEY: 3'UTR  
LOCATION: 2502..3260  
US-08-323-460A-1



Query Match 37.3%; Score 1955.6; DB 2; Length 3260;  
Best Local Similarity 82.7%; Pred. No. 0;  
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

QY 1996 TAACTCTCTGCGCAGATTAGGCGGAAAGATCAAACTTCAGAGACTTCCAGCCAGTT 2055  
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QY 2116 TCACACTGTGTGAACTGTCCAAAGCCAAAGAGAGATTGGCAGTTGGCAGAGAAATA 2175  
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QY 2176 CTAAAGCTGGATCCATGGTATGTGTGTGATGTATGTCTTAATTTGATCTTGA 2235  
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QY 2296 CTGTGTGGAATTTCTCTGCTGAATTTTATCTCATATTTGTCACTGATGTTTCAAA 2355  
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DB 540 TCCAGTTCCACTCACTCACTCAGCAGAGATGTCGCGCGCTGTGATGGCTATTCAGAGATG 599  
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DB 600 GAAATTTGCGAGAGCCATCCAGTTGGGCGTAGAAGACACTGTGATGGGATCAAGAGAG- 658  
QY 2656 TTTCTGAGGACATCTGTCCCAACAATATCTGAAACCAAGAGAACTGCTCCCTGAG 2715  
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QY 2776 TCAGAGGACATTTCTGAGAGACTGGCCAGCATTTCACTAGAGACCTTTAGTTCAACACA 2835  
DB 768 TCAGAGGACATTTCTGAGAGACTGGCCAGCATTTCTGAGAGACTTTCCAGCT----- 819  
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DB 820 -----CAACAACAACAAGAGAGCAACCAAGCAATGTTTAAACAAAAGGACAGCCAC 872  
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QY 3136 CCACTCTTTACTCAGTCAAGACCTTTCCTCCAGTAATATACAGAGCCAAAGCCATCT 3195  
DB 1095 CCACTCTTTACTCAGTCAAGACCTTTCCTCCAGTAATATACAGAGCCAAAGCCATCTC 1154  
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DB 1155 CGACCCCTTCCGGCACTCAAGCAAACTAGGGGACCCCAAAAAATAGCATGACACTT 1214  
QY 3256 GATCTGAACAGTAGTTCCTCAATGATGATGACAGCTTGGCTGTACCATATAGATAT 3315  
DB 1215 GATCTGGGCAAGTCTTCCAGAGTGTGACGACAGCTTTTGGCGGCGGCAACAGTGGCAAC 1274  
QY 3316 GCTGTATTAACCCAGTCAAGAGACAGTCTTCAACCCAGTACAGAGAAATCAGATTAAT 3375  
DB 1275 GCGGTATTAACCCAGTCAAGAGAGAGTCTTCAACCCAGTGGAGCAAGTGAATTAAT 1334  
QY 3376 GTCAATACAGAGTCAACTCAGTATTTGAGAGCTTCTTGAAGCATTTATGCTTCAAGT 3435  
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QY 3436 GATCAACAGTAACTTTAATGTCAGAGTGTCTGCTCTCTGAAAAGGCTGAAAT 3495  
DB 1395 GACACGACAGTCACTTTCAAGTCCGAAGTGGCGCTCTCTCGGAAAAGGCCGAAAT 1454  
QY 3496 GATGATACCTCAAAAGATGATGTAATCATTAATCAAAAGTGCAGAAAGATGGAAGCT 3555  
DB 1455 GACACACCTCAAAAGAGAGAGCTCAATCATTAATCAAAAGTGCAGAAAGATGGAAGCT 1514  
QY 3556 GAAGAAAGAGAGGTTTAAAGCAATTTGCAATGTCACAGCTTCAGAGATGCCCTCCC 3615  
DB 1515 GAAGAGAGAGAGGTTTAAAGCAATTTGCAATGTCACAGCTTCAGAGATGCCCTCCC 1574  
QY 3616 ATAGTTCTCAGCTGACAGTTGAAAATGAGAAATATCATTTATTTCAACAGATACA 3675  
DB 1575 ATGCTCCTCAGCTGACAGTTGAAAATGAGAAATATCATTTATTTCAACAGAGACACA 1634  
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DB 1635 CCAGAAACTCTTCCAGAGATACCAAAAGCAAAACAGCTTACAGAGAGAGAGCTGATGG 1694  
QY 3736 CTGAAAGGTCAACAGATAGGCTTGGAGCATTTTCTTCTGTATTCAGGCTCAAGATGTG 3795  
DB 1695 CTGAAAGGCGAGAGATAGGCTTGGAGCATTTTCTTCTGTATTCAGAGAGAGAGATGTG 1754  
QY 3796 GGAAGTGAATTTAATGAGCTGTTAAACAGGTGACTTATGTCAGAAACACATCTTCTGAG 3855  
DB 1755 GGGAGTGGAGCTTTAATGAGCTGTTAAACAGGTGACTTATGTCAGAAACACATCTTCTGAG 1814  
QY 3856 CAAGAGAAGTGTAGAGAGCACTAAGAGAGATGAAGATGAATGATGACCACTCTGAATCAT 3915  
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QY 3916 CCAAAACATTAATGAGTGTGGAGCCACGCTGAGAGAGCAATTTCAATCTTCTTAT 3975  
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QY 3976 GAATGATGAGGAGGAGTGGTGTCTCATTTTGTGATTAATTTGAGAGCTTCAAGAA 4035  
DB 1935 GAGTGAATGAGGAGGAGATGCTGTGCTCAGCTTGTGATTAATTTGAGAGCTTCAAGAG 1994  
QY 4036 TCACTAGTTAATTAATCACTGAACAGTACTCTCGTGGCTTGTATCTCATGAAGAAC 4095  
DB 1995 TCACTGTCTTAATTAATCACTGAACAGTACTCTCGTGGCTTGTATCTCATGAAGAAC 2054  
QY 4096 CAATCATTAACAGAGATGTCAAAGGTCCAATTTGTAATTTGACACACTGTGTCAGAGAC 4155  
DB 4155 CAATCATTAACAGAGATGTCAAAGGTCCAATTTGTAATTTGACACACTGTGTCAGAGAC 4214

Db 2055 CAGATCATTCACAGAGACGTCAAGGTGGCAACCTGCTCATTTGACAGCACCGGTGACAGG 2114  
OY 4136 CTAAGAAATTCAGAAATTTGGAGCTCGACGCAAGTTGGCATCAAAAGAAATGTTGACAGA 4215  
Db 2115 CTGAAATTCAGAAATTTGGAGCTCGACGCAAGTTGGCATCAAAAGAAATGTTGACAGA 2174  
OY 4216 GAGTTTCAGAGGCAATTTACTGGGACAAATTCATTTATGCGACCTGAGTACTAAGAGGT 4275  
Db 2175 GAGTTTCAGAGGCAATTTACTGGGACAAATTCATTTATGCGACCTGAGTACTAAGAGGT 2234  
OY 4276 CAACAGTATGAGAGAGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4335  
Db 2235 CAGCAGTATGAGAGAGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2294  
OY 4336 TGTGCAAAACCACTGCAATGCAAGCAAAACCACTGCAATGCAATGCAATGCAATGCAATGCA 4395  
Db 2295 TGTGCAAAACCACTGCAATGCAAGCAAAACCACTGCAATGCAATGCAATGCAATGCAATGCA 2354  
OY 4396 ATTGCTAGTCAAGTCACTGCTCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4455  
Db 2355 ATTGCTAGTCAAGTCACTGCTCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2414  
OY 4456 GTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4515  
Db 2415 GTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2474  
OY 4516 AAGCATCCAGTCTTTCGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4575  
Db 2475 AAGCATCCAGTCTTTCGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2534  
OY 4576 AAGATGCTCAACAG 4631  
Db 2535 AAGATGCTCAACAG 2594  
OY 4632 CCATGATGCTCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 4691  
Db 2595 CCCTCAGCGCACTGAACAGCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2653  
OY 4692 ATTGCAAAATCATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 4750  
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OY 4751 ACTGTAACGTGCTTTCGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4810  
Db 2714 ACTGTAACGTGCTTTCGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2773  
OY 4811 CATGATTAATTCAGAAAGCATTAATTTATTTTGGAGCACTTTTTCAGCAA 4864  
Db 2774 CATGATTAATTCAGAAAGCATTAATTTATTTTGGAGCACTTTTTCAGCCTA 2825

RESULT 8  
US-08-461-146C-1  
Sequence 1, Application US/08461146C  
Patent No. 5981265  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, GARY L.  
TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lathive and Cockfield  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,146C

FILED DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/354,516  
FILED DATE: 21-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/049,254  
FILED DATE: 15-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/323,460  
FILED DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/11690  
FILED DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04178  
FILED DATE: 15-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KARA, Catherine J.  
REGISTRATION NUMBER: P41,106  
TELECOMMUNICATION INFORMATION:  
REFERENCE/DOCKET NUMBER: CPI-004CN3  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3260 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MEKK  
STRAIN: murine  
IMMEDIATE SOURCE:  
LIBRARY: mouse liver  
CLONE: MEKK CDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..485  
NAME/KEY: CDS  
LOCATION: 486..2501  
NAME/KEY: 3'UTR  
LOCATION: 2502..3260  
US-08-461-146C-1

Query Match 37.3%; Score 1955.6; DB 2; Length 3260;  
Best Local Similarity 82.7%; Pred. No. 0;  
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

OY 1996 TATACCTCTTGGCAGAGTTAGCGAAGAAAGATCAAACTTCAGAGACTTCCAGCAGTT 2055  
Db 1 TACACTCTTGGCAGAGTTAGCGAAGAAAGATCAAACTTCAGAGACTTCCAGCAGTT 60  
OY 2056 GTAGACACCATCTAGTCAATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 2115  
Db 61 GTAGACACTATCTTGTCAAGTGTGAGAT -CCAACAGCCGACAGAGTCACTGTGCAATA 119  
OY 2116 TCAACAGCTTGGAACTGTGCAAAAGCCCAAGCAGAGAGTGTGCAAGTGTGCAAGAAATA 2175  
Db 120 TCTACAGTGTGAACTGTGCAAAAGCCCAAGCAGAGAGTGTGCAAGTGTGCAAGAAATA 179  
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QY 2656 TTCTTGAGGCACTGTCTCCCAACAATATCTGGAAGAAACACAGAGACATTTCCCTGAG 2715  
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Db 708 CACACAGTCCATTAGAGAAACTGAAAGATATGCTCTACAAATTTAGTGCAGT 767  
QY 2776 TCAGAGACATTTCTGAGAGACTGGCCAGCATTTTCAGTAGAGACCTTCTACTGAACACA 2835  
Db 768 TCGAGAGACATTTCTGAGAGACTGGCCAGCATTTTCAGTAGAGACCTTCTACTGAACACA 819  
QY 2836 ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 2895  
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QY 2896 AGTCAGTGTGTAAGTCTCTCTCTTATCTCATCATTCCTCAATTAATGTTCCAGCTTG 2955  
Db 873 AGTCAGTGTGTAAGTCTCTCTCTTATCTCATCATTCCTCAATTAATGTTCCAGCTTG 929  
QY 2956 TCACACCCCTTCT 3015  
Db 930 TCAGCCCTTCT 974  
QY 3016 CATAGACTTCAGGAGATTCATCTCCCTGAGAAATACCTTCTGATCTCTCTCAAAACACAGC 3075  
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QY 3376 GTCAATACAGAGTCAACATCTGATATGAGACCTTCTTAAGATCTATGCTTCAAGT 3435  
Db 1335 GTCAATACAGAGTCAACATCTGATATGAGACCTTCTTAAGATCTATGCTTCAAGT 3495  
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Db 1395 GATACCAACAGTATTTAATGATGAGAAATGCTGTCTCTCTCTCTCTCTCTCTCTCTCT 1454  
QY 3496 GATGATACCTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3555  
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QY 3736 CTGAAAGTCAACAGATGAGGCTTGGACATTTCTCTTATATCAGGCTCAAGATGTG 3795  
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Db 1875 CCAACATCAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1934  
QY 3976 GAATGATGAGGAGGAGTGGTGGCTCATTTGCTGATGATGATGATGATGATGATGATGAT 4035  
Db 1935 GAATGATGAGGAGGAGTGGTGGCTCATTTGCTGATGATGATGATGATGATGATGATGAT 1994  
QY 4036 TCAGTACTTATTAATCACTACAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4095  
Db 1995 TCAGTACTTATTAATCACTACAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2054  
QY 4096 CAATCAATCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4155  
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QY 4156 CTAAAGATGAGATTTTGGAGCTGACAGAGTGGCATCAAAAGAGACGTGGTGCAGAG 4215  
Db 2115 CTAAAGATGAGATTTTGGAGCTGACAGAGTGGCATCAAAAGAGACGTGGTGCAGAG 2174  
QY 4216 GAGTTTAAAGGACATTAATGATGAGGACATTTGATGATGATGATGATGATGATGATGAT 4275  
Db 2175 GAGTTTAAAGGACATTAATGATGAGGACATTTGATGATGATGATGATGATGATGATGAT 2234  
QY 4276 CAACAGATGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4335  
Db 2235 CAACAGATGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2294  
QY 4336 TGTGCAAAACACCATGGAATGAGAAACACATCAATCATCTTGTGATATTAAG 4395  
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QY 4396 ATTGCTAGTCACTACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGAT 4455  
Db 2355 ATTGCTAGTCACTACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGAT 2414  
QY 4456 GTGGCTCTGCTGTTTGAATCAACCTCAGAGACAGCTCCATCAAGAGAGCTCTG 4515  
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QY 4516 AAGCATCCAGTCTTTCGTAATGATGACCAATTTATGACATCACTACAGTAGAANC 4575  
DB 2475 AAACATCCGCTTCCTCCGTAACGACGTAAGTAATGTTTCAGATCAGCTATAGAGAC 2534  
QY 4576 AGGATGCTCAACAGAAAAAACTTGS---TGCGAACAACATGATATTTCTACGTG 4631  
DB 2535 AGGATATGAAACCGGAGAGAGAAAAAGAACTTTGTGGCGACATGCGCTACACGACG 2594  
QY 4632 CCATGATGCCACTGTAAGAGCTATGTAAGAGAGGCGCACTGTGGGAAACCTTACCTAAGATGTG 4691  
DB 2595 CCTCAGCGCACTGAAACGCGAGAAAGGCGGAGGAGAA--CGTACTTAAGCATGTG 2653  
QY 4692 ATTGACAAATCATGATCTGTACTTAAGCTACATATGCA--AAAGCCAAACTGTGAGAA 4750  
DB 2654 ATTGACAAATCATGACCTGTACTTAAGCTACATATGCAACATCATACAGCTGTGAGAA 2713  
QY 4751 ACTGAACTGCTCTTCAAGAACTGCGCTAGGTGTAAGAAACAAATGAAGTTTG 4810  
DB 2714 ACTGCAACCGCTCTTCAAGAGACTGCTGTGGGAGCAAGAAAGCGCATGAGATTG 2773  
QY 4811 CATGACTAAATTTGCAAGAGCAATATTTTGTGGAGCACTTTTCAGCAA 4864  
DB 2774 CATGACTAAGAAAGAGCAATAAATTTA--TTTTGGAGCACTTTTCAGCTA 2825

## RESULT 9

US-08-461-145C-1

Sequence 1, Application US/08461145C

Patent No. 6074861

GENERAL INFORMATION:

APPLICANT: JOHNSON, GARY L.

TITLE OF INVENTION: NOVEL MERK PROTEINS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lathive and Cockfield, LLP

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,145C

FILING DATE: 5-JUNE-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/049,254

FILING DATE: 11-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/323,460

FILING DATE: 14-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/11690

FILING DATE: 14-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/04178

FILING DATE: 15-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/354,516

FILING DATE: 21-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kara, Catherine J.

REGISTRATION NUMBER: P-41,106

REFERENCE/DOCKET NUMBER: CPI-004CNI

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3260 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MERK  
STRAIN: murine  
IMMEDIATE SOURCE:  
LIBRARY: mouse liver  
CLONE: MERK CDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..485  
NAME/KEY: CDS  
LOCATION: 486..2501  
NAME/KEY: 3'UTR  
LOCATION: 2502..3260  
US-08-461-145C-1

Query Match 37.3%; Score 1955.6; DB 3; Length 3260;

Best Local Similarity 82.7%; Pred. No. 0;

Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

QY 1996 TATACCTCTTGGCAGAGTTAGCGAAAGATCAAACTTCAGAGACTTCTCCAGCAGTT 2055  
DB 1 TACACTCCTTGGCAGAGTTAGCGAAAGATCAAACTTCAGAGACTTCTCCAGCAGTT 60  
QY 2056 GTAGACACCATCTTGTCAATGTGCAATGCAATAGCCGACAGATCAGCTGTCCATA 2115  
DB 61 GTAGACACCATCTTGTCAATGTGCAAT--CCAAAGCCGACAGATCAGCTGTCCATA 119  
QY 2116 TCAACAGCTTGGAGCTGTGCAAGAGGCAAGAGAGAGTGGCAGTGGCAGAAATA 2175  
DB 120 TCTACAGTGTGCAAGCTGTGCAAGAGGCAAGAGAGAGTGGCAGTGGCAGAAATA 179  
QY 2176 CTAAAGCTGTGATCCATGTGATGTGCTGTGATGTATGCTTAAATGTATCTTGTGA 2235  
DB 180 CTAAAGCTGTGATCCATGTGATGTGCTGTGATGTATGCTTAAATGTATCTTGTGA 239  
QY 2236 AACCAATGATCAAACTTGGCAGAGACTTGTGGCCGCTTGTCTTATGATAGA 2295  
DB 240 AACCAATGATCAAACTTGGCAGAGACTTGTGGCCGCTTGTCTTATGATAGA 299  
QY 2296 CTTGTTGGGAATTCCTGCTGAATTTATCCTCAATTTGCAATGATGATGTTCCACA 2355  
DB 300 TTGCTGTTGGGAATTCCTGCTGAATTTATCCTCAATTTGCAATGATGATGTTCCACA 359  
QY 2356 GCTGAGCCGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2415  
DB 360 GCTGAGCCGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419  
QY 2416 TCCATTGATTAATCCCACTCAATGTTGGCAAACTTTCAGAGAGATCTACTTGAGTCT 2475  
DB 420 TCCATTGATTAATCCCACTCAATGTTGGCAAACTTTCAGAGAGATCTACTTGAGTCT 479  
QY 2476 GCAAGATGATTAATCAAGTACCACTGATGTTTCAAACTTGAATGATGATGATGATGAT 2535  
DB 480 GCAAGATGATTAATCAAGTACCACTGATGTTTCAAACTTGAATGATGATGATGATGAT 539  
QY 2536 TCCAGTTCCACTCACTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2595  
DB 540 TCCAGTTCCACTCACTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 599  
QY 2596 GAAATTTCCGAAAGCATCCAGTGTGGCGGTAGAGAACTTTGATGATGATGATGATGAT 2655  
DB 600 GAAATTTCCGAAAGCATCCAGTGTGGCGGTAGAGAACTTTGATGATGATGATGATGAT 658  
QY 2656 TTCTTGGAGGATCTGTGTTCCCAACATATCTGGAACCAAGAGAAAGATTTCCCTGAG 2715



RESULT 10  
US-08-628-829-1  
; Sequence 1, Application US/0862829A  
; Patent No. 6333170  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Gary L.  
; TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To External  
; FILE REFERENCE: CPI-004DVEP3  
; CURRENT APPLICATION NUMBER: US/08/628,829A  
; EARLIER FILING DATE: 1996-04-05  
; EARLIER APPLICATION NUMBER: 08/440,421  
; EARLIER FILING DATE: 1995-05-15  
; EARLIER APPLICATION NUMBER: 08/323,460  
; EARLIER FILING DATE: 1994-10-14  
; EARLIER APPLICATION NUMBER: 08/049,254  
; EARLIER FILING DATE: 1993-05-15  
; EARLIER APPLICATION NUMBER: 08/410,602  
; EARLIER FILING DATE: 1995-04-24  
; EARLIER APPLICATION NUMBER: 08/472,934  
; EARLIER FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3260  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (486)..(2501)  
; US-08-628-829-1

Query Match 37.3%; Score 1955.6; DB 4; Length 3260;  
Best Local Similarity 82.7%; Pred. No. 0;  
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

QY 1996 TTTACTCTTGGCAGCTTTAGCGGAAAGATCAAACTTCAGAGCTTCCAGCCAGTT 2055  
DB 1 TTTACTCTTGGCAGCTTTAGCGGAAAGATCAAACTTCAGAGCTTCCAGCCAGTT 60  
QY 2056 GTAGACACCATCTTGTCAATGATGCGATGCGCAATGCGCAATGCGATGCGCAAT 2115  
DB 61 GTAGACACCATCTTGTCAATGATGCGATGCGCAATGCGCAATGCGATGCGCAAT 119  
QY 2116 TCAACCTTTGGAGCTGTGCAAGGCGCAAGAGAGAGTGGCAGTTGGCAGAGAAAT 2175  
DB 120 TCTACGTCTGTGAGCTGTGCAAGGCGCAAGAGAGAGTGGCAGTTGGCAGAGAAAT 179  
QY 2176 CTTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2235  
DB 180 CTTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 239  
QY 2236 AACCAAACTGATCAAACTGATGATGATGATGATGATGATGATGATGATGATGAT 2295  
DB 240 AACCAAACTGATCAAACTGATGATGATGATGATGATGATGATGATGATGATGAT 239  
QY 2296 CTTGTTTGGAGTTTCTGATTTTCTGATTTTCTGATTTTCTGATTTTCTGATTT 2355  
DB 300 CTTGTTTGGAGTTTCTGATTTTCTGATTTTCTGATTTTCTGATTTTCTGATTT 359  
QY 2356 GCTGAGCTGTTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2415  
DB 360 GCTGAGCTGTTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419  
QY 2416 TCCATTGATTAATCCACTCAATGATGATGATGATGATGATGATGATGATGATGAT 2475  
DB 420 TCCATTGATTAATCCACTCAATGATGATGATGATGATGATGATGATGATGATGAT 479  
QY 2476 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2535  
DB 480 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539  
QY 2536 TCCAGTTCACATCTTCAACGAGATGATGATGATGATGATGATGATGATGATGAT 2595

DB 540 TCTGGCTCCACCCACTTCAACAGATGCGCGCGCTGTGATGCTATGCGGATGAGATA 599  
QY 2596 GAAATTTGCCAGAGCATTCGAGTGGGCGTGAAGACACTTTGGATGCAAGGACAG 2655  
DB 600 GAAATTTGCCAGAGCATTCGAGTGGGCGTGAAGACACTTTGGATGCAAGGACAG 658  
QY 2656 TTTCTGAGGAGCATCTGTTCCCAAACTATCTGAAACCAAGAGACAGAGTCCCTGAG 2715  
DB 659 -CTTACAGAGCGTGGCGCCCAACAGCTGTCT-AGAAAAGAGCTCCCTTGAAG 707  
QY 2716 TGCAGAGTCCATTAGAGAAAAGTGAAGAGTTATGCTATCAAAATTTGAGTGCAGT 2775  
DB 708 CACACAGTCCATTAGAGAAAAGTGAAGAGTTATGCTATCAAAATTTGAGTGCAGT 767  
QY 2776 TCAAGAGACTTTCTGAGAGACTGGCAGAGACTTCAAGTGGAGACTTCTGATCAACACA 2835  
DB 768 TCGAGAGACTTTCTGAGAGACTGGCAGAGACTTCAAGTGGAGACTTCTGATCAACACA 819  
QY 2836 ACAACAAACAACAAGAGAGCAACCAAGGATGTTCAACAAAGAGAGAGAGAG 2895  
DB 820 -CAACAAACAACAAGAGAGCAACCAAGGATGTTCAACAAAGAGAGAGAGAGAG 872  
QY 2896 AGTCAAGTGTGAGAGTCTCTCTTATCTCATCATTTCCCAATTAATGTTTCCAGCTTGG 2955  
DB 873 AGTCAAGTGTGAGAGTCTCTCTTATCTCATCATTTCCCAATTAATGTTTCCAGCTTGG 929  
QY 2956 TCAACCCCTTCTCTTCTACCCCATCTGTACAGAGTGGAGACTGCAACAGATGCTTAG 3015  
DB 930 TCAAGCCCTTGTCT 974  
QY 3016 CATAGACTTCAAGAGATTCATTCCTGCAAGATTCCTGCAATCTCTCTCAACACAGCC 3075  
DB 975 CACAGAGCCCAAGAGATTCATTCCTGCAAGATTCCTGCAATCTCTCTCAACACAGCC 1034  
QY 3076 AAGTTTCTCTCAATTTCCAGAGAACTGCTGAAACCAAGAGTCAATTAATCTTTC 3135  
DB 1035 AAGTTTCTCTCAATTTCCAGAGAACTGCTGAAACCAAGAGTCAATTAATCTTTC 1094  
QY 3136 CCAAGCTTACTAGTCAAGAGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3195  
DB 1095 CCAAGCTTACTAGTCAAGAGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1154  
QY 3196 AGACCTACCCAGAGTATCAAGTAAACAGGAGATCTCTCAAAAATAGATGACATTT 3255  
DB 1155 AGACCTACCCAGAGTATCAAGTAAACAGGAGATCTCTCAAAAATAGATGACATTT 1214  
QY 3256 GATCTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3315  
DB 1215 GATCTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1274  
QY 3316 GCTGTTATACCCAGTACAGAGAGAGTGTACACCCAGTGAAGAGAGAAATGATGAT 3375  
DB 1275 GCTGTTATACCCAGTACAGAGAGAGTGTACACCCAGTGAAGAGAGAAATGATGAT 1334  
QY 3376 GTCAATACAGAGTCAATCTCAATTTGAGAGACTTCTTGAAGCATCTATGCTTCAAGT 3435  
DB 1335 GTCAATACAGAGTCAATCTCAATTTGAGAGACTTCTTGAAGCATCTATGCTTCAAGT 1394  
QY 3436 GATACAGAGTAACTTTAAGTACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 3495  
DB 1395 GATACAGAGTAACTTTAAGTACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1454  
QY 3496 GATGATACCTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3555  
DB 1455 GATGATACCTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1514  
QY 3556 GAAAGAGAGAGAGTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 3615  
DB 1515 GAAAGAGAGAGAGTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1574  
QY 3616 ATAGTTCCTACAGTGTGAGTGAAGATGAGAGATGATGATGATGATGATGATGAT 3675

Db 1575 ATGTCCTCAGCTGAGGTGGAATAATGGAGATATTTATCATTCATGACGAGACACA 1634  
Qy 3676 CCAGAGACTCTTACAGGACATACCAAGCAAAACCGATATAGAGAAGACACTGAATGG 3735  
Db 1635 CCAGAAACTCTTCCAGACATACCAAGCGAAACACCTTACAGAGAAAGACGTGAGTGG 1694  
Qy 3736 CTGAAAGCTCAACAGATAGGCTTGGAGCATTTCTTCTTGTATACAGGTCAAGATGTG 3795  
Db 1695 CTGAAAGCGCAGCAGATAGGCTTGGAGCATTTCTTCTTGTATACAGGTCAAGATGTG 1754  
Qy 3796 GGAATGTAACCTTTAATGCGCTTTAAACAGGTGATGATGATGAGAAACACATCTTTCAG 3855  
Db 1755 GGGACTGGGACTTAAATGCTGTGAAACAGGTACGTAGCTCAGAAACACATCTTCGAG 1814  
Qy 3856 CAAGAAGAACTAGTACAGACCTAAGAGAAGATAGATAGATGAGCCATCTGAATCAT 3915  
Db 1815 CAGAGAGAGGTGTGAGAGCTTGAAGAGATCCGATGAGGTGACCTCAACCAT 1874  
Qy 3916 CCAAAAGTCAATGATGATGTTGGAGCCGTGTGAGAAAGCAATTAACATCTTTCAT 3975  
Db 1875 CCAAAAGTCAATGATGATGTTGGAGCCGTGTGAGAAAGCAATTAACATCTTTCAT 1934  
Qy 3976 GAATGATGGCAGGAGGATCGGTCTATTTGCTGATTAATGAGGCTTCAAGAA 4035  
Db 1935 GAGTGGATGGCGGAGGATCTGTGCTCAGCTTGTAGTAAATACGAGCTTCAAGAG 1994  
Qy 4036 TCAGTAGTATTAATACATGACATGAAACGATTAATGAGGCTTTCATTCATGA 4095  
Db 1995 TCAGTGTATTAATACATGACATGAAACGATTAATGAGGCTTTCATTCATGA 2054  
Qy 4096 CAATATTCACAGATATGCAAAAGTGCCAAATTTGCTAATGACAGCATCTGTGAGAGA 4155  
Db 2055 CAATATTCACAGATATGCAAAAGTGCCAAATTTGCTAATGACAGCATCTGTGAGAGA 2114  
Qy 4156 CTAGAGATTTGCAATTTTGGAGCTGACAGCGAGTGGCATCAAAAGGAGTGTGACAGA 4215  
Db 2115 CTAGAGATTTGCAATTTTGGAGCTGACAGCGAGTGGCATCAAAAGGAGTGTGACAGA 2174  
Qy 4216 GAGTTTCAGGACAAATTAATGAGGAGCAATTCATTAATGAGCAGTGAATGAAGAT 4275  
Db 2175 GAGTTTCAGGAGCAATTAATGAGGAGCAATTCATTAATGAGCAGTGAATGAAGAT 2234  
Qy 4276 CAACATGATGAGAGAGCTGTATGATGAGAGTGTGCTGTATTAAGAAATGGCT 4335  
Db 2235 CAACATGATGAGAGAGCTGTATGATGAGAGTGTGCTGTATTAAGAAATGGCT 2294  
Qy 4336 TGTGCAAAACCACTGATGAGAAACCACTCCATCATCTGCTTGTATTAAG 4395  
Db 2295 TGTGCAAAACCACTGATGAGAAACCACTCCATCATCTGCTTGTATTAAG 2354  
Qy 4396 ATTTGATGCAACTACTGCTCATGATCCCTTCAATTTGCTGCTTGTATTAAGAT 4455  
Db 2355 ATTTGATGCAACTACTGCTCATGATCCCTTCAATTTGCTGCTTGTATTAAGAT 2414  
Qy 4456 GTGGCTCTTGTGTTTGAACCTTCAACCTCAGAGACAGCTCATCAAGAGCTACTG 4515  
Db 2415 GTGGCTCTTGTGTTTGAACCTTCAACCTCAGAGACAGCTCATCAAGAGCTACTG 2474  
Qy 4516 AAGCATCAGCTTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 4575  
Db 2475 AAGCATCAGCTTCTTGTATGATGATGATGATGATGATGATGATGATGATGATG 2534  
Qy 4576 AGGATGCTCAACAAGAAAAAACTG---TGGGAAACAATGATGATGATGATGATG 4631  
Db 2535 AGGATGCTCAACAAGAAAAAACTG---TGGGAAACAATGATGATGATGATGATG 2594  
Qy 4632 CCATGATGCTCAACAAGAAAAAACTG---TGGGAAACAATGATGATGATGATGATG 4691  
Db 2595 CCATGATGCTCAACAAGAAAAAACTG---TGGGAAACAATGATGATGATGATGATG 2653  
Qy 4692 ATTTGCAAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4750  
Db 2654 ATTTGCAAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2713

Qy 4751 ACTGTAACCTGTGCTTCAAGAACTGCGCTTGTGAGTGAACAGAAACATGATGTTG 4810  
Db 2714 ACTGTAACCTGTGCTTCAAGAACTGCGCTTGTGAGTGAACAGAAACATGATGTTG 2773  
Qy 4811 CATGACTAATGCAAGACATATTTATTTTGGAGCACTTTTCAGCA 4864  
Db 2774 CATGACTAATGCAAGACATATTTA--TTTGGAGCACTTTTCAGCTA 2825

RESULT 11  
US-08-472-934-11  
Sequence 11, Application US/08472934  
Patent No. 575346  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, GARY L.  
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lohive and Cockfield  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,934  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/440,421  
FILING DATE: 15-May-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/354,516  
FILING DATE: 21-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 5,405,941  
FILING DATE: 15-Apr-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/323,460  
FILING DATE: 14-Oct-1994  
PRIOR APPLICATION DATA: PCT/US94/11690  
FILING DATE: 14-Oct-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04178  
FILING DATE: 15-Apr-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Giulio A. Deconceli, Jr. Esq.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: CPI-004DVC2  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2503 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 466..2325  
US-08-472-934-11

Query Match 1.4%; Score 75.8; DB 1; Length 2503;



Best Local Similarity 48.2%; Pred. No. 2.1e-08;  
Matches 336; Conservative 0; Mismatches 352; Indels 9; Gaps 4;

3666 ACAGATACACAGAGAGACTTACACAGAGACATACCAAGCAAAACCAACCTATAGAGAGA 3725  
1464 AGACAACTCTACTTTGACGTGACAGACATCAAGCCACCCAGCCGTACCTCGAGCTCC 1523  
3726 CACTGATGCGTGAAGGTCACAGATAGCCCTTGAGAGCAATTTCTTCTTATCAGGC 3785  
1524 GACCAACTGGAGACTGGAGCAAGCTCTTGCCAGAGAGCTTTGGAGGGCTACCTCG 1583  
3786 TCAAGATGGGAGACTGAGCACTTAAAGCTTAAACAGGACTATAGTCAGAAACAC 3845  
1584 CTATGATGTGATACCGGAGAGAGACTGGCTGTAAAGCAAGTTCAAGTTACCTGAGG 1643  
3846 ATCTTCTGAGCAAGAGAGAGAGAGCACTAAGAGAGAGATTAAGATATGAGCA 3905  
1644 CCCAGAGACCAAGAGAGAGATTAAGCACTTATGATGTGAATTCAGTTTGAAGAACTT 1703  
3906 TCTGAATCATCCAA-ACATCATTTAGAGAGTTGGAGCCAGCTGTGAGAGCAATTTACA 3964  
1704 GTTGATGAGCAATTTGCTACATATATGCTGTTGAGAGATCCCTCAGAGAGAAACACT 1763  
3965 ATC--TCTTCATTTAGATGAGAGGGGAGATCGGTGCTCATTTGCTAGTAAATATGG 4022  
1764 TTCCATCTTTATGAGATATATCCAGGGGGTTCAATTAAGCAACATAAAGCCTACGG 1823  
4023 AGCCTTCAAGAGATAGTATTAATTAACACTGACAGCACTGACCGGCTTTCGTA 4082  
1824 AGCTTTACTGAGAGAGTACAGAGAGAGTACACCGCTGATTCGAGAGGGGCTCATTA 1883  
4083 TCTCATGAAAAACCAATCATTCACAGAGATGTCAAGAGTGCCTAATTTCTAATTCAGAC 4142  
1884 TTTGATATGATATATGATGCTCAGATAGATATCAAGAGAGCAATATCTTTAAGGATTC 1943  
4143 CACTGGTCAGACTAAGATTTGAGATTTGAGCTGAGAGAGAGTGGCTGCAAAAG 4202  
1944 CACAGGCAATATC--AAGTTAGAGACTTTGGGCTAGTAAAGGCTTGAACACTCT 2001  
4203 AACTGTGAGAGAGATTTGAGAGCAATTTACTGGGAGCAATTTGATTTAGCACTTGA 4262  
2002 CTCTAGGAGACAGAAAT---GAGTCTGTACAGAGGACGCACTGATGATGCTGCTA 2057  
4263 GGTACTAGAGGTCAACAGTATAGAGAGAGCTGTGATGATGATGATGCTGCTGCTAT 4322  
2058 GGTCTATCATGTGAGAGAGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2117  
4323 TATGAAATGGCTGTGCAAAACCAACATGAGATGCA 4359  
2118 GGTAAATGCTAAGTGAAGAGCACTTTGGGCTGAA 2154

Db

RESULT 12  
US-08-461-146C-11  
Sequence 11, Application US/08461146C  
Patent No. 5981265  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, GARY L.  
TITLE OF INVENTION: METHODS FOR REGULATING MEK PROTEIN ACTIVITY  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lahlive and Cockfield  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,146C  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/354,516  
FILING DATE: 21-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/049,254  
FILING DATE: 15-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/323,460  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/11690  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04178  
FILING DATE: 15-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KARA, Catherine J.  
REGISTRATION NUMBER: P41,106  
REFERENCE/DOCKET NUMBER: CPT-004CN3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2503 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 466..2325  
US-08-461-146C-11

Query Match 1.4%; Score 75.8; DB 2; Length 2503;  
Best Local Similarity 48.2%; Pred. No. 2.1e-08;  
Matches 336; Conservative 0; Mismatches 352; Indels 9; Gaps 4;

3666 ACAGATACACAGAGAGACTTACACAGAGACATACCAAGCAAAACCAACCTATAGAGAGA 3725  
1464 AGACAACTCTACTTTGACGTGACAGACATCAAGCCACCCAGCCGTACCTCGAGCTCC 1523  
3726 CACTGATGCGTGAAGGTCACAGATAGCCCTTGAGAGCAATTTCTTCTTATCAGGC 3785  
1524 GACCAACTGGAGACTGGAGCAAGCTCTTGCCAGAGAGCTTTGGAGGGCTACCTCG 1583  
3786 TCAAGATGGGAGACTGGAACCTTAAATGAGCTTTAAACAGGTGACTTATGTCAGAAACAC 3845  
1584 CTATGATGTGATACCGGAGAGAGAGCTGCTGTTAAGCAAGTTCAAGTTAAGCTGAGAG 1643  
3846 ATCTTCTGAGCAAGAGAGAGAGAGCACTAAGAGAGAGATTAAGATATGAGCA 3905  
1644 CCCAGAGACCAAGAGAGAGATTAAGCACTTATGATGTGAATTCAGTTTGAAGAACTT 1703  
3906 TCTGAATCATCCAA-ACATCATTTAGAGAGTTGGAGCCAGCTGTGAGAGCAATTTACA 3964  
1764 TTCCATCTTTATGAGATATATCCAGGGGGTTCAATTAAGAGCAACATAAAGCCTACGG 1823  
4023 AGCCTTCAAGAGATAGTATTAATTAACACTGACAGCACTGACCGGCTTTCGTA 4082  
1824 AGCTTTACTGAGAGAGTACAGAGAGAGTACACCGCTGATTCGAGAGGGGCTCATTA 1883  
4083 TCTCATGAAAAACCAATCATTCACAGAGATGTCAAGAGTGCCTAATTTCTAATTCAGAC 4142  
1884 TTTGATATGATATATGATGCTCAGATAGATATCAAGAGAGCAATATCTTTAAGGATTC 1943



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OY 4143 CACGGGTCAGAGACTAAGAAATTCACATTTTGGAGCTGAGCCAGGCTTGGCATCAAAAGG 4202
Db 1344 CACAGGCAATATC--AAGTTAGAGACCTTTGGGGGCTAGTAACGGCTTCAGACCACTCTGT 2001
OY 4203 AACTGATGCAGAGAGATTTCAGGGACAAATTAAGTGGGACAAATTAATGATTTATGGCACTGA 4262
Db 2002 CTCACAGACAGCAAGAAAT---GAAATCTGTGCACAGGACAGCCCAATCACTGGATAGATGTCGA 2057
OY 4263 GGTCCTAAGAGGCTCAACAGTATGGAAGAGAGCTGTATGTATGAGATGTTGGCTGTCTAT 4322
Db 2058 GGTCATCAGTGGGAAAGGCTATGTGGAAGAAAGCAGACATCTGAGATGTAGCATGTACTGT 2117
OY 4323 TATGAAATGCTGTGGCAAAACACCACTAGATGCA 4359
Db 2118 GGTAAATGCTACTGTAATAAGCCACCTTGGGCTGAA 2154

RESULT 13
US-08-461-145C-11
Sequence 11, Application US/08461145C
Patent No. 6074861
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: NOVEL MEKK PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461.145C
FILING DATE: 5-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 11-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,460
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/354,516
FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: P-41,106
REFERENCE/DOCKET NUMBER: CPT-004CNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ. ID NO.: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 466..2325

```

US-08-461-145C-11

Query Match 1.4% ; Score 75.8; DB 3; Length 2503;  
Best Local Similarity 48.2%; Pred. No. 2.1e-08;  
Matches 336; Conservative 0; Mismatches 352; Indels 9; Gaps 4;

OY 3666 ACAGGATACACCAGAGACTCTCACAGGACATACCAAGCAAAACAACCGTTTACAGAAGA 3725  
|| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1464 AGACAATCTTACTTTGATGTGCACAGACATCAGCCACCCGCCGTCCTACCTCAGACTCC 1523  
OY 3726 CACTGAATGGCTGGAAGGTCACAGATFAGGCTTGAGACATTTTCTTCTTTATCATAGGC 3785  
|| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1524 GACCACCTGGAGACTGGGCAAGCTGCTTGCGCAAGAGACCTTTTGGTAGGGCTTACCTG 1583  
OY 3786 TCAAGATGTGGGAATCGAAGCTTAATGCTGTATAAACAGGTGACTTATGTACAGAAAC 3845  
|| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1584 CTATGATGTGATACCGGAGAGAGAGCTGCTGTTAAGCAAGTTCAAGTTAACCTTGAGAG 1643  
OY 3846 ATCTTCTGACGACAGAAGAGTAGTAGAAGCCTAAGAGAAAGATTAAGATGATGAGCCA 3905  
|| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1644 CCCAGAGACACGACGAAGGAAGTAATGCACTTGAGTGTGMAATTGACTGTGGAAAACTT 1703  
OY 3906 TCTGATCATCTCAA -ACATCATTTAGGATGTTGGGAGCAGCTGTGAGAGAACTTAACA 3964  
|| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1704 GTTGCAATGAGCAATTTGCTCAGTATATGCTGTTTGAAGGATCCTCAGGAAAACACT 1763  
OY 3965 ATC--TCTTCAATTGATGATGGCAGGGGGATCGGTGGCTCATTTTGTGATTAATATG 4022  
|| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1764 TTCCATCTTTATGGAGTATATGCCAGGGGGTTCAATTAAAGCAACATAAAGCTACGG 1823  
OY 4023 AGCCTTCAAGAAATCAGTAGTTAATTAACACTACGTAAACAGTTACTCCGTGGCCTTTCGTA 4082  
|| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1824 AGCTCTTACTAGAAACGTGACGAGGAAGTACACCCGTCAGATTCGTGAGGGGGTCCATTYA 1883  
OY 4083 TCTCATAAAAACCAATATCATTTCAAGAGATGTCAAAAGGTGCCAATTTGTAATTGACAG 4142  
|| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1884 TTTGCATAGTAATATGATGATTTGCCATAGAAATATCAAAAGGCAAAATATCTTAAGCGATTC 1943  
OY 4143 CACTGTGACGAGACTAACAATATTCAGATTTTGGAGCTGCACACCAGTTGGCATCAAAAG 4202  
|| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1944 CACAGGCAATATTC--AGTTAGSAGACTTTGGGGCTAGTAAGCGCTTCACAGACATCTGT 2001  
OY 4203 AACTGTGTCAGAGAGAGTTTCAAGGACAAATTACTGGGCAAAFTGCATTTATGSCACTGA 4262  
|| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 2002 CTCACGACACAGGAAAT---GAAGTCTGTACAGGCAAGCCATACGTAGATGATCCTCGA 2057  
OY 4263 GGTACTAGAGGTCAACAGTATGGAAGSAGSGTGTGATGTATAGAGTGTGTGCTGTAT 4322  
|| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 2058 GGTACTAGGTGAGAGAGGCTATGGAAGAAAGACAGACATCTGTAGATGTACTGT 2117  
OY 4323 TATGAAATGGCTTGTGCAAAACACACCATGAGATGCA 4359  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 2118 GGTAGAAATGCTACTAGAAAAGCCACTTGGGCTGAA 2154

RESULT 14  
US-08-829-7  
Sequence 7, Application US/08628829A  
Patent No. 6333170  
GENERAL INFORMATION:  
APPLICANT: Johnson, Gary L.  
TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To External Factors  
FILE REFERENCE: CFI-004DPCP3  
CURRENT APPLICATION NUMBER: US/08/628,829A  
CURRENT FILING DATE: 1996-04-05  
EARLIER APPLICATION NUMBER: 08/440,421  
EARLIER FILING DATE: 1995-05-15  
EARLIER APPLICATION NUMBER: 08/323,460  
EARLIER FILING DATE: 1994-10-14  
EARLIER APPLICATION NUMBER: 08/049,254  
EARLIER FILING DATE: 1993-05-15  
EARLIER APPLICATION NUMBER: 08/410,602  
EARLIER FILING DATE: 1995-04-24

EARLIER APPLICATION NUMBER: 08/472,934  
EARLIER FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 2503  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (466)..(2322)  
US-08-628-829-7

Query Match 1.4%, Score 75.8; DB 4; Length 2503;  
Best Local Similarity 48.2%; Pred. No. 2.1e-08;  
Matches 336; Conservative 0; Mismatches 352; Indels 9; Gaps 4;

QY 3666 ACAGGATACACGAGACTCTACACGAGACATACCAAAACAAACCGTATAGAGAGCA 3725  
DB 1464 AGACATCCCTACTTTCGCTCAGACATCAGACATCCACCCACCCGCTTACCTGAGCTCC 1523  
QY 3726 CACTGATGCGTGAAGGTCAACAGATAGCCCTTGAGCATTTCTCTTGTATCAGGC 3785  
DB 1524 GACCAACTGGAGACTGGGCAAGCTCTTGCCCAAGAGCTTTGGTAGGCTTACTCTG 1583  
QY 3786 TCAGATGCGAGACTGCACTTTAATGCGTGTAAACAGTGAATATGTCAGAAACAC 3845  
DB 1584 CTATGATGTTGATACCGAAGAGAGCTGCTTTAAGCAAGTTACGTTAACCTGAGAG 1643  
QY 3846 ATCTTCTGAGCAAGAGAGTAGTAGCACTAAGAGAGATTAAGAGATATAGCA 3905  
DB 1644 CCCAGAGACCAAGAGAGAGATTAAGCACTGAGTGTGAATTCAGTTGTAAAACTT 1703  
QY 3906 TCTGATCATCCCA-ACATCATTAGAGATGTTGGAGCCACGTTGAGAGCAATTTACA 3964  
DB 1704 GTTGATGAGCAATTTGCTGATTTATGCGTGTGAGGAGATCCGACAGAGAAACACT 1763  
QY 3965 ATC--TCTTCAATGATGATGCGAGGAGATCGTGGCTCATTTGCTGAGTAAATGCG 4022  
DB 1764 TTCCATCTTTATGAGTATATGCGAGGGGTTCAATTAAGCACTAAAGCCTACGG 1823  
QY 4023 AGCCCTCAAGATCAGTATTAATACATACACATGACATTAACCCGCTTCCGTA 4082  
DB 1824 AGCTTTCTGAGAGAGGAGAGAGAGTACCCGTCAGATTTGAGAGGGGCTCCATTA 1883  
QY 4083 TCTCATGAAAAACCAATCATTCACAGAGATGTCAAAGGTGCCAATTTGCTAATTGACAG 4142  
DB 1884 TTTGATGATGATATATGATGTTCCATAGAGATATCAAGAGCAATTTATCTTAAGGATTC 1943  
QY 4143 CACTGCTCAGAGACTTAAGATTTGCAATTTGAGACTGCAAGCCAGGTTGGCATCAAAAG 4202  
DB 1944 CACAGGCAATATC--TAGTTAGGAGACTTTGGGCTAGTAAAGGCTTCAGACCATCTGT 2001  
QY 4203 AACGTCGAGAGAGTTTACGGGCAATTTACTGGGACAATTTGATTTATGAGCCATGA 4262  
DB 2002 CTCTAGGCAACGCAAT-----GAAGTGTCTACAGGACAGCCCATCTGAGATGCTGA 2057  
QY 4263 GGTACTAAGAGGTCAACAGATGAGAGAGCTGTGATGATGAGTGTGGCTGTAT 4322  
DB 2058 GGTATCAGTGGAGAGAGCTATGAGAAAGAACAGACATCTGAGATGTAAGCATGTACTGT 2117  
QY 4323 TATAGAAATGCTTGCAGAAACCAACCATGCAATGCA 4359  
DB 2118 GGTAGAAATGCTAAGTAAAGCCACCTTGGGCTGAA 2154

RESULT 15  
US-09-359-757-1  
Sequence 1, Application US/09359757  
Patent No. 6080546  
GENERAL INFORMATION:  
APPLICANT: Brett P. Montia  
APPLICANT: William Gaarde

APPLICANT: Lex M. Cowser  
TITLE OF INVENTION: ANTISENSE MODULATION OF MEK5 EXPRESSION  
FILE REFERENCE: RTS-0078  
CURRENT APPLICATION NUMBER: US/09/359,757  
CURRENT FILING DATE: 1999-07-23  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 1  
LENGTH: 5236  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (361)..(4485)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 4687  
OTHER INFORMATION: unknown  
US-09-359-757-1

Query Match 1.4%, Score 74.4; DB 3; Length 5236;  
Best Local Similarity 50.4%; Pred. No. 6.6e-08;  
Matches 245; Conservative 0; Mismatches 226; Indels 15; Gaps 2;

QY 3883 GAAGAGATTAAGATATGAGCATCTGAATCATCCAAACATCATTAAGATGTTGGAGCC 3942  
DB 2530 GAAGAAATAGCATTCATTAACACCTGAAGCAGCAAAATATGTCAGTATCTGGCTCT 2589  
QY 3943 ACGTGAAGAGAGCAATTAACATCTTCATTTAATGATGAGGAGGAGATCGGTGCT 4002  
DB 2590 TTCACTGAGAAATGCTTTTATTAATCTTCATGAGAGAGGCTCCGAGAGAGTCTTCT 2649  
QY 4003 CATTTGCTGATTAATATG-----AGCCTTCAAGAAATCAGTATTAATTAACATAC 4053  
DB 2650 GCTCTCTGCTTCCAAATGGGCTCATTAAGACAAATGAGCAAAATGCGTTTAT 2709  
QY 4054 ACTGAACATTAATCTGCGTGGCTTTGATGTCCTGATGAGAAACCAATATTCACAGAGAT 4113  
DB 2710 ACAAAGCAATTAATGGAAGATTAATAATATCTCCATGACAAATCAGATGTTCCCGGAG 2769  
QY 4114 GTCNAAGTGCCAATTTGCTAATGACAGACCTGTCAGAGACTAAGATGACAGATTTT 4173  
DB 2770 ATAAAGGTGACAAATGTTGATTAATTAATCTTAAGATGTTGTTCTAAGATCTCTGACTTC 2829  
QY 4174 GAGCTGACAGCCAGTGGCATCAAAAGAACTGTCAGAGAGAGTTCAGGACAAATTA 4233  
DB 2830 GGAACATCAAAAGAGGCTTGCTGATTAACCCCTGACTGAATTTACTGTACCTTC 2889  
QY 4234 CTGGGAGCAATTTGCTTTATGACCTGAGTACTTAAGAGTCAACACATATGGAAGAGC 4293  
DB 2890 CAGTATATGGCACCAAGAAATTAATAGATAAGGACCAAGAG-----CTACGGAAGAGCA 2943  
QY 4294 TGTGATGATGAGAGTGGCTGCTGCTAATTAATAGAAAGCTTGTGCAAAACCATGAG 4353  
DB 2944 GCAAGCATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3003  
QY 4354 AATGCA 4359  
DB 3004 TATGAA 3009

Search completed: December 27, 2002, 22:19:40  
Job time : 303 secs